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Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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DFNWEYPESKHQHKKLVNRDLKTOSGSEMKKFLSTLTIDGYTRSDQGLYTCAASSGLM
TKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVUD
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SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQK
SLSLSPGR"
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CQ774324 Sequence
CQ790351 Sequence
CQ816433 Sequence
AX594307 Sequence
AX616608 Sequence
AX616908 Sequence
AX56699 Sequence
AX5699 Sequence
AX70958 Sequence
AX70958 Sequence
AX70958 Sequence
BD01334 Novel pep
BD01334 Novel pep
BD01336 Novel pep
BD01336 Sequence
AX65284 Sequence
AX01386 Sequence
AR01340 Novel pep
BD01336 Sequence
AR0169284 Sequence
AR076262 Sequence
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papadopoulos, N.J., Davis, S. and Yancopoulos, G.D. Modified chimeric polypeptides with improved pharmacokinetic
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100.0%; Pred. No. 6.2e-310;
iive 0; Mismatches 0;

    1377
    note="unnamed protein product"

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AX556959
AX709558
AX556949
AX709548
BD013334
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AB159728
AR031186
AR042591
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BD013338
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AR300619
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AR108867
E10697
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Best Local Similarity 100.
Matches 1377; Conservative
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      DEFINITION
ACCESSION
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KEYWORDS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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AX056749
LOCUS
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AXO56741 Sequence
AXO56737 Sequence
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AX338256 Sequence
AX138158 Sequence
AR112718 Sequence
AX556168 Sequence
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AX17115 Sequence
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AR173440 Sequence
CQ857740 Sequence
AX357970 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                  1 atggtcagctactgggacac......ccctgtctccgggtaaatga 1377
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                              - nucleic search, using sw model
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Gaps

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Result ş

	1453 bp DNA linear PAT 17-JAN-2 9724	arrhini, Hominidae carchini, Hominidae carcopoulos,G.D. ith improved pharma (US)	/organism="Homo sapiens" //o_Lype="unassigned DNA" //db_xref="taxon:9606" 691445 //codon_start=1 //codon_start=1 //protein_id="CAC22377.1" //pro	NSTEVRVHEKGREGBKTHTCPPCPARELLGGSVFLEPPKKOTLMISKTPETTCVVVD VSHEDPEVKENMYDGVETHORFREEGYNSTYRVVSVLTVLHODMLNGKEYKCKV SNKALPAPIEKTISKAKGOPREPQVYTLPPSRBEITKNQVSLTCLVKGFYPSDIAVEM ESNGOPERNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGRVVFSCSVMHEALHNYTQK SLSLSPGK"	Duery Match 96.5%; Score 1328.4; DB 6; Length 1453; Best Local Similarity 98.6%; Pred. No. 1.3e-298; Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 1 ATGGTCAGCTACTGGGACACCGGGGTCCTGTGGGGGCTGCTCAGTGTCTCTCTC	DD 69 ATGGTCAGCTACTGGGACACCGGGGCTGCTGGCTGCTGCTGCTTCTC 128	Db 180 CCCGAAATTATACACATGAAGGAAGGGAGGTCGTCATTCCCTGCCGGGTTACGTCA 239
ATGGTCAGCTACTGGGACCCGGGGTCCTGTGCGCGCTGCTCAGCTGTCTGCTCCTCC 60	301 GGGCTTCTGACCTGTGAACAGTCAATGGGCATTTGTATAAGACAACTATCTCACA 360	421 TCTGTTGGGAAAAGCTTGTCTTAATTGTACGCAAGAACTGAACTAATGTGGGGATT 480 481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATAAGAAACTTGAACTGAACGAAC		ACCTCATGATCTCCCGGACCCCTGAGGTCACATGCTGGTGGTGGTGGACGTGGACGTGGACGTGAGGTGGACGTGAGGTGGACGTGAGGTGGACGTGGACGTGAGCTGGACGTGGACGTGGACGTGGACGTGGACGTGGACGTGGTGGTGGTGGTGGTGGACGTGAGGTGGACGGAC	GACCCTGAGGTCAAGTTCAACTGGTGGCGCGTGGGGGTGCTAATGCCAAGACA AAGCCGCGCGGAGGAGCATACAACTGGTACCGTGTGGTGGTCAGCGTCCACGTCCTC	961 CACCAGGARTGGCTGAATGGCAGGAGTGAAGTCCAACAAGAGCCTCCCA 1020 961 CACCAGGACTGGATGGCAAGGAGTACAAGTGCAACAAGAGCCTCCCA 1020 961 CACCAGGACTGGATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCTCCCA 1020 1021 GCCCCCATCGAAAAACCATCTCCCAAAGGCCAGCCCCCGAGAACCACAGGTGTAC 1080	1081 ACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG

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EATVNGHLYKTNYLTHRQTNTIIDIQLLPRKSLELLVGEKLVLNCTVWAEFNSGVTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDYPCKQAERCKWVPERRSQCTHTELSSILTIHNVSQHDLGSYVCKANNGIQRFREST
EVIVHENGPGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPBVTCVVDDVSH
EDEDYKFNWYDGVEYHNAKTKPRESDXNSTYRVVSYLTVLHQDMLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                     GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
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Modified chimeric polypeptides with improved pharmacokinetic
properties
Patent: WO 0075319-A 13 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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69. .1436
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BNNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSF
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Properties
Patent: WO 0075319-A 7 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers 1. .1389 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /proteIn_id="CAC22375.1" /db_xref="GI:12309721" Query Match
Best Local Similarity 85.5%;
Matches 1201; Conservative 61 ACAGGATCTAGTTCCGGA 412 481 셤 ò

Papadopoulos, N.J., Davis, S. and Yancopoulos, G.D. Modified chimeric polypeptides with improved pharmacokinetic

properties
Patent: WO 0075319-A 3 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers

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/note="unnamed protein product"
/codon_start=1

/protein_id="CAC22373.1" /db_xref="GI:12309717"

/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 1. .1674

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                                                                                                                                                                                                                                                                      71.7%; Score 987.4; DB 6;
86.1%; Pred. No. 3.6e-219;
ive 0; Mismatches 171;
                                                                                                                                                                                                                                                                                             Local Similarity 86.1
nes 1119; Conservative
                                                                                                                                                                                                                                                                                                                       Matches 1119;
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PAT 17-JAN-2001

linear

DNA

Sequence 3 from Patent W00075319.
AX056737.1 GI:12309716

RESULT 6
AX056737
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

sapiens (human)

Homo

ORGANISM

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1

318 624 378

564

438 744 498 804 558 860 618 918 678

684

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GFYSCKYLAVPTSKKKETESAIYIFISDTGRPFVEMYSEIPEIIHWTEGRELVIPCRV
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                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                       Length 1704;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                     71.3%; Score 982.4; DB 6;
85.4%; Pred. No. 5.3e-218;
iive 0; Mismatches 161;
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Matches 1132; Conserv
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     GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 1035
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                                                    CCCGTGCTGGACTCCGACGACTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC
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Modified chimeric polypeptides with improved pharmacokinetic
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Properties
Patent: WO 0075319-A 9 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAC22376.1"
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Sequence 9 from Patent WO0075319.
AX056743
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TSPYSCKYLAUVPSKKETPSAIY IF ISDTGRPFVBWS SEI PET IHWTEGREL VI PCRV
TSPYSCKYLAUVPSKKETPSAIY IF ISDTGRPFVBWS SEI PET IHWTEGREL VI PCRV
TSPNITVOTLKKRPDJDLI PDGRR I IWDSRKGFI ISNATYKET GELITCCBATWOHLI VKR
NYLTHROTNTI I DVOI STPRPVKLLRGHTLVINCTATTPLNTRVOMTWSYPDEKNKRA
SVRR ID DSWISHANI PYSVLTI DKOMONOGAL YTCRVRSGEPSFRSVNTSVPSVHI YDKAGP
GEPKSCDKTHTCPPCTAPELLGGESVEL, PPRKPOTLANI SRTPEVTCVVDVSHEDDE
VKRNWYVDGVEVHNGAKTRPREEQNNSTYRVVSVLTVLHODMLNGKEYKCKVSNKALPA
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/db_xref="GI:12309715"
/translation="MVSYWDTGVLLCALLSCLLLTGSSSGSKLKDPELSLKGTQHIMQ
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PATENT: WO 0075319-A 1 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
LOCATION/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 1 from Patent W00075319.
AX056735 AX056735.1 GI:12309714
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Mammalia; Eutheria; Primates;
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Unclassified.

E 1 (bases 1 to 2043)

AS Greve,J.M. and McClelland,A.

Antiviral methods

Antiviral methods

AL Patent: US 6130202-A 14 10-OCT-2000;

Location/Qualifiers

2043 """known"
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Pred. No. 6e-149;
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Sequence 14 from patent US 6130202.
AR112718
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Best Local Similarity 95.9%;
Matches 704; Conservative
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                 GCCCTCCCAGCCCCCATCGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAAGCAA
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GCCCTCCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA
                                                         CAGGTGTACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCTGACC
                                                                        CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="fusion of human cDNA and Fc tag coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roczniak,S., Dubois-Stringfellow,N.A. and Zolotorev,A. Method of regulating angiogenesis using ryk protein Patent: WO 0185789-A 17 15-NOV-2001; Bayer Corporation (US)
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Pred. No. 3.1e-149;
0; Mismatches 3;
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synthetic construct
other sequences; artificial sequences.
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Sequence 17 from Patent W00185789.
AX338526
AX338526.1 GI:18128935
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Best Local Similarity 99.6%;
Matches 689; Conservative
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/translation="MCHLWFPLLLVAAPRWVLSEPKSCDKTHTCPPCPAPELLGGPSV PLPPPKPTLMISRTPEVTCVVUDVSHEDPEVKFWYYDGVEVHUNKTKFREEGYNS TRYVGVYLTVHQDWINGREPKTKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVERESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVWHBALHNHYTQKSLSLSPGK"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            CGTGTGGTCAGCGTCCTCACCGTCCTGCACGGACTGGATGGCAAGGAGTACAAG
                                                                                                                                                                                                   365 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG
    GCCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC
                      GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGGAGGAGGAGTACAACAGCACGTAC
                                                                                                                                          GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG
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100.0%; Pred. No. 1.6e-148;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
7. .762
/note="unnamed protein product"
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Sequence 17 from Patent WO0238766.
AX556168
AX556168.1 GI:25899545
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/db_xref="G1:25899546"
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1610 GCGTCCTCACCGTCCTGCACCAGGACTGCCTGAATGGCAAGGACTACAAGTGCAAGGTCT 1669
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                                              GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT
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Cocks B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 1223 19-AUG-2003;
Location/Qualifiers
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49.7%; Score 684; DB 6; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 684; Conservative 0; Mismatches 0; Indels
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AR380678
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (bases 1 to 1019)
E. 1 ao, W., Wong, S., Hickey, W.F., Hammang, J.P. and Baetge, E.E.

Cell surface molecule-induced macrophage activation

L. Patent: JP 2002528078-A 1 03-SEP-2002;

NEUROTECH SA

OS Homo sapiens (human)

PN 12 1002528078-A/1

PD 03-SEP-2002

PF 21-OCT-1999 JP 2000578449

PR 22-OCT-1999 US 09/178869

PI WENG TAO, SHOU WONG, WILLIAM F. HICKEY, JOSEPH P. HAMMANG, EDWARD E.

PI BAETGE
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                  TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGGACCCCTGAGGTCACA
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Cell surface molecule-induced macrophage activation.
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                                                    Unclassified.
Unclassified.
1 (bases 1 to 1019)
1 (bases 1 to 1019)
1 Tao, W., Wong, S., Hickey, W.F., Hammang, J.P. and Baetge, E.Edward.
Cell surface molecule-induced macrophage activation
Patent: US 6197294 1 06-MAR-2001;
Location/Qualifiers
GACAAAACTCACACACAGCCCAGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC
                    GACAAAACTCACACACATGCCCACCGTGCCCAGCACCTTGAGGGGGGGACCGTCAGTC
                                                                                                           TGCGTGGTGGTGGACGTGAGGCCCTGAGGTCAAGTTCAACTGGTACGTGGAC
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100.0%; Pred. No. 1.7e-148;
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Sequence 1 from patent US 6197294.
AR137115 GI:14478624
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/organism="unknown"
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Best Local Similarity 100.
Matches 684; Conservative
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                                                                                                                     Unclassified.

1 (bases 1 to 1019)

Tao, W., Wong, S., Hickey, W.F., Hammang, J.P. and Baetge, E.E.
Cell surface molecule-induced macrophage activation
Patent: US 656691-A 1 14-JAN-2003;
                                                                                                                                                                                                                                                                       Length 1019;
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                                 DNA
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1 from patent US 6506891.

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    /organism="unknown"
    /mol_type="genomic DNA"

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                                            Sequence
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AG1P1/16, ..., no.1K9/48, AG1K38/00, AG1K39/395, AG1K48/00, AG1P1/04, 1
PC AG1P3/10, AG1P7/06, AG1P9/02, AG1P11/02, AG1P11/06, AG1P17/00, PC
PC AG1P19/02, AG1P21/02, AG1P21/04, AG1P25/nn ....
PC AG1P37/06,
PC AG1P37/06,
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1. 1019
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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(c) 1993 - 2005 Compugen Ltd.
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US-10-811-170-1 1377 Title: Perfect score: Sequence:

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IDENTITY NUC Gapox 10.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	f	TD	AAA91076	ABQ74610	AAA91074	ABQ74608	AAA91075	ABQ74609	AAA91071	ABQ74605	AAA91072	ABQ74606	AAA91070	ABQ74604	AAA91073	ABQ74607	AAA91077	ABQ74603	AAL56122	AD010510	AAL56123	ADO10512
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ALIGNMENTS

Flt1 receptor fusion protein VEGFR1R2-FcDeltaC2 (a) coding sequence. Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region; ss. /*tag= a /product= "VEGFR1R2-FcDeltaC2(a)" Location/Qualifiers 1. .1377 /*tag= a AAA91076 standard; DNA; 1377 BP. (first entry) WO200075319-A1 Unidentified 05-APR-2001 14-DEC-2000. AAA91076; RESULT 1 AAA91076 Key

23-MAY-2000; 2000WO-US014142.

99US-0138133P 08-JUN-1999;

(REGE-) REGENERON PHARM INC.

Davis S, Yancopoulos GD; Papadopoulos NJ,

WPI; 2001-071076/08. P-PSDB; AAY97596.

Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model

Claim 9; Fig 24; 159pp; English.

This sequence encodes a fusion protein of the invention between the Flt1

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1020 1020 1080 1080 1140 1200 1200 1260

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CTCACCGTGGACAAGAGCAGGTGGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
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     AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCCTCACCGTCCTG
                      AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGGTCAGCGTCCTCACCGTCCTG
                                                           CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA
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receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular
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                                                                                                                                                     to the mammal or human. A VEGF antagonist has antipsoriatic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypetide to decrease or inhibit plasma leakage and used in making the polypetide to decrease or inhibit plasma leakage and
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                                                                                                          present invention describes a method for treating psoriasis and
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                s and enhancing wound healing in humans comprises
a vascular endothelial cell growth factor (VEGF)
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                                                                          Example 20; Fig 24A-C; 179pp; English
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Matches 1377; Conservative
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                                                                                                                                Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, rephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes a fusion protein of the invention between the Flt1 receptor and the Fc region of igG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                            receptor fusion protein Flt1D2.VEGFR3D3.fcDeltaC1(a) DNA sequence
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                                                                                                                                                                                                                                                                                  receptor; fusion protein; chimeric protein; pharmacokinetic;
na leakage; vascular permeability; IgG Fc region; ss.
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Pred. No. 1.8e-244;
0; Mismatches 158;
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                                                                        standard; DNA; 1444
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Best Local Similarity 86.7%;
Matches 1201; Conservative
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B
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                                                                                                                                                                                            psoriasis; wound healing; Flt1 receptor; antipsoriatic; antinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeablility; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic,
                                                                                                                                                     Modified Flt1 receptor Flt1D2.VEGFR3D3.FcDELTAC1(a) nucleotide sequence
                                                                                                                                                                               Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
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Pred. No. 1.8e-244;
0; Mismatches 158; Indels
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/*tag= a
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                                                                    standard; cDNA; 1444
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Best Local Similarity 86.7%;
Matches 1201; Conservative
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                                                         Length 1359;
                             Sequence 1359 BP; 381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;
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                                                       Score 1039; DB 5;
Pred. No. 5.3e-242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                      TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGGAGGAATGGGCAG
                                                                                                                                              1251 ccedadadaacaacracaadaaccacecrccerecresaacrcceacescrccrrcrrcrrc
                                                                                                                                                                                                       1311 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
                                                          TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGCAATGGGCAG
                  CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC
                                                                                                                                                                            TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGGAACGTCTTCTCATGCTCC
                                                                                                                                                                                                                                                     GIGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGT
                                                                                                                                                                                                                                      GTGATGCATGAGGCTCTGCACACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor fusion protein Mut2:Flt1(2-3deltaB)-Fc coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region; ss.
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960 942 961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCA 1020

Example 12; Fig 14A-C; 179pp; English.

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AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGGAATGGGCAGCCGGAGAAC 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF) antagonist.
                                                                                                                  AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG
                                                                                     GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VECF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antiarthritic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, rephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VECF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), ashown, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes Mut2:Flil(2-3 delta B)-Fc which is used in an example from the present invention
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This sequence encodes a fusion protein of the invention between the Flt1 receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
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                                                                                                                                                                              Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 GACTICAACTGGGAATACCCTICTTCGAAGCATCAGCATAAGAAACTIGTAAACCGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        586 ATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1389 BP; 394 A; 393 C; 322 G; 280 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1032.4; DB 5
Pred. No. 2.2e-240;
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(REGE-) REGENERON PHARM INC
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Matches 1201; Conservative
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Location/Qualifiers
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Matches 1201; Conservative
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                                                                                                                                                                                                                                                                               TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053
                                                                                                                                                                                                                                                                                                       1006 TGCAAGGTCTCCAACAAGCCCTCCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;. postrasis; antinidal healing; Flt1 receptor; antipaciatic; antinidal amnatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration; diabetic retinopathy; gene; see
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                                                 TTCCTCTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
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                                                                                   TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
                                                                                                                                 TGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC
                                                                                                                                                         TGCGTGGTGGTGGACGTGAGCCACGAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC
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                                    GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAACTCCTGGGGGGACCGTCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutation 3 Flt1(2-3)-Fc nucleotide sequence.
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enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antiposoriatic, antiantlammatory, vulnerary, antiaethmatic, antirheumatic, antiarthumatic, nephrotropic and ophthalmological activities. The method can be used in verating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes Mut3:Flt1(2-3)-Fc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ACAGGATCTAGTTCCGGA-----GGTAGACCTTTCGTAGAGATGTACAGAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for treating psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1032.4; DB 6; Length 1389;
Pred. No. 2.2e-240;
0; Mismatches 161; Indels 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1389 BP; 394 A; 393 C; 322 G; 280 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which is used in an example from the present invention
"Mut3:Flt1(2-3)-Fc protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; Fig 15A-C; 179pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yancopoulos GD;
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                                                                                                                                                       Flt1 receptor fusion protein Mut1:Flt1(1-3deltaB)-Fc coding sequence.
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Best Local Similarity 86.1%;
Matches 1119; Conservative
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (WGGF) antagonist to the mammal or human. A VEGF antiachmatic, antinflammatory, vulnerary, antiachmatic, antinflammatory, vulnerary, antiachmatic, antinflammatory, vulnerary, antiachmatic, antinflammatory, vulnerary, antiachmatic, antinflammatory, by the method is also useful in treating psoriasis and enhancing wound healing in humans by administering ver antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumator) as such as a brain oedema associated with inflammatory disorders (e.g. rheumator) as age-related asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes Mutil:FlL(1.3 celta B)-Fc which is used in an example from the present invention
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                                                                                                                                                                           psoriasis, wound healing; Flt1 receptor; antipsoriatic; antiinflāmmatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological, vascular permeability; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration; diabetic retinopathy; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 ACTGAAGGAAGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
                                                                                                                                                        Human, Flt1; vascular endothelial growth factor, VEGF; VEGF antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCCGAAATTATACACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Mutl:Flt1(1-3 delta B)-Fc protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;
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                                                                                                                  Mutation 1 Flt1(1-3 delta B)-Fc nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 987.4; DB 6;
Pred. No. 1.9e-229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2001; 2001US-00773877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGE-) REGENERON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI: 2002-608488/65.
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     1516 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes a fusion protein of the invention between the Plt1 receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                             1576 AGGTGGCAGCAGGAGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACACCAC
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                                                                                                                                                                                                                                                                                                                                                                                           fusion protein, chimeric protein; pharmacokinetic, vascular permeability; IgG Fc region; ss.
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                                                                                                                                                                                                                                                                                                                                                       receptor fusion protein Mut4:Flt1(1-3R-N)-Fc coding
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                                                                                                              Score 982.4; DB 5;
Pred. No. 3.2e-228;
0; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Flt1(1-3R-N)-Fc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davis S, Yancopoulos GD;
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                                                                                                                                                                                                                                            AAA91073 standard; DNA; 1704
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Best Local Similarity 85.4%;
Matches 1132; Conservative
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                                                                                                                                                                                                                                                                                                                     (first entry)
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P-PSDB; AAY97593.
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                                                                                                                                                                                                                                                                                                                                                                                                              plasma leakage;
                                                                                                                                                                                                                                                                                                                                                                                             receptor;
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TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT
                                                                                   TTAAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory discorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related
                                                                                                                                                                                                                                                                                                                                                                   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist; postrasis; wound healing; Flt1 receptor; antipostratic; antinflammatory; vulnerary; antiasthmatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; oedema; inflammation; asthma; bain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration; diabetic retinopathy; gene; ss.
                                    1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
                                                                          GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
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macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage or vascular permeability. The present sequence encodes Mut4:Flt1(2-3 >N)-Fc which is used in an example from the present invention
                                                                                                                         Gaps
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                                                                                            Score 982.4; DB 6; Length 1704; Pred. No. 3.2e-228; 0; Mismatches 161; Indels 33;
                                                                   Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;
                                                                                             Query Match
71.3%;
Best Local Similarity 85.4%;
Matches 1132; Conservative (
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This sequence encodes a fusion protein of the invention between the Flt1 receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
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GenCore version 5.1.6
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OM nucleic + nucleic search, using sw model

September 23, 2005, 13:12:56 ; Search time 4299 Seconds (without alignments) 12192.254 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-811-170-1 1377 1 atggtcagctactgggacac......ccctgtctccgggtaaatga 1377

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

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68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: 90 est1: *
2: 90 est1: *
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6: 90 est5: *
7: 90 est6: *
7: 90 est6: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	BG753979 602709506	BQ708975 AGENCOURT	BQ712021 AGENCOURT	BM007897 603617582	BQ709152 AGENCOURT	4	CR595172 full-leng	CR612308 full-leng	CR604961 full-leng	CR616804 full-leng	CR626477 full-leng	CR612813 full-leng	CR601777 full-leng	CR625051 full-leng	CRS95194 full-leng	4	CR613460 full-leng	_	CR598548 full-leng	CR614200 full-leng	CR619687 full-leng	CR606782 full-leng	CR593349 full-leng	CR618075 full-leng
SUMMARIES		ΩI	BG753979	BQ708975	BQ712021	BM007897	BQ709152	CR611254	CR595172	CR612308	CR604961	CR616804	CR626477	CR612813	CR601777	CR625051	CR595194	CR591904	CR613460	CR620071	CR598548	CR614200	CR619687	CR606782	CR593349	CR618075
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d	Query	Match	49.7	49.7	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.6
		Score	684	684	683	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4	682.4
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ORIGIN

CR613511 full-leng CR619868 full-leng	-	CR598462 full-leng	CR598316 full-leng	CR607277 full-leng	CR611016 full-leng	CR594000 full-leng	BX346946 BX346946	BQ706204 AGENCOURT	BQ709339 AGENCOURT	BQ709771 AGENCOURT		BQ709144 AGENCOURT	BG674795 602620925	BQ712363 AGENCOURT	BQ711291 AGENCOURT	BG397723 602438784	BM008412 603617406	BX367600 BX367600	BQ709859 AGENCOURT
CR613511 CR619868	CR611468	1 CR598462	I CR598316	I CR607277	1 CR611016	1 CR594000	BX346946	5 BQ706204	5 BQ709339	5 BQ709771	5 BX360518	5 BQ709144	BG674795	5 BQ712363	5 BQ711291	BG397723	BM008412	BX367600	BQ709859
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49.6	49.6	49.6	49.6	49.6	49.6	49.6	49.5	49.5	49.4	49.3	49.2	49.2	49.1	49.1	49.1	48.8	48.8	48.8	48.8
682.4	682.4	682.4	682.4	682.4	682.4	682.4	681.4	681.4	680.8	679.2	677	6.929	676.6	676.6	929	672	672	671.8	671.4
25 26	27	28	29	30	31	32	33	34	35	36	c 37	38	39	40	41	42	43	C 44	45

ALIGNMENTS

BG753979 BG709506F1 NIH_MGC_48 Homo samena sequence. BG753979 BG753979.1 GI:14064632 BG7.600 sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human)	Talmatara; Elleria; Filmaters; Caraillill; Nomilliage; Nomo. 1 (Dases 1 to 871) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Lind Hong/Rubin Laboratory	cDNA Lik DNA Seq Clone di Clone di found thi http://in Plate: Li High qual	/tissue_type="primary B-cells from tonsils (cell line)" /lab_host="MHIDB (phage-resistant)" /clone_lib="NIH_MGC 48" /clone_lib="NIH_MGC 48" /note="Organ: B-cells, Vector: porB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the pirectionally cloned into ECORI/XhoI sites using the following S' adaptor: GCCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
RESULT 1 BG753979 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOURCE	7,510

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/note="organ: spleen; Vector: poTB7; Site_1: Site_2:
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov k column: 12
Plate: LLCM3469 row: k column: 12
High quality sequence stop: 604.
Location/Qualifiers
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AGENCOURT 8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
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I (bases 1 to 983)
II (Marc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
49.7%; Score 684; DB 4; L6
100.0%; Pred. No. 4.7e-179;
ive 0; Mismatches 0;
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/note=_Organ: spleen; vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI; tDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGA(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superseript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
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I (bases 1 to 843)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                             1114 AACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
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/db_xref="taxon:9606"
/clone="IMAGE:6281403"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: Xhol; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into BcoR1/Xhol sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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E 1 (bases 1 to 941)

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

COLLON GONA Library Preparation: Rubin
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8418162 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6281403
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                                 CTCTCCCTGTCTCCGGGTAAATGA 707
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Homo sapiens
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequenoming by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: m column: 22
High quality sequence stop: 739.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.6%; Score 682.4; DB 5; Best Local Similarity 99.9%; Pred. No. 1.3e-178; Matches 683; Conservative 0; Mismatches 1;
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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-8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 925)
1 (bases 1 to 925)
1 (hases 1 to 925)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                             GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGAACTCCTGAGTC
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                                                Score 682.4; DB 4;
Pred. No. 1.3e-178;
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoP V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

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full-length cDNA clone CSODI040YA16 of Placenta Cot 25-normalized
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                  803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGCTGGACTCC
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                                            GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG
                                                                                                                              1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCCAGCGACATCGCCGTGGAG
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/mol_type="mRNA"
/mol_txef="taxon:9606"
/clone="CSOD1040YA16"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Homo sapiens (human)
Homo sapiens
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Matches 683; Conserv
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                                                                                                                                                                                       CR611254 1022 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DE007XJ17 of Placenta of Homo sapiens
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648 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAGAAGAGC 707
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/plasmid="pCMVSPORT_6"
                                            1377
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/db_xref="taxon:9606"
/clone="CS0DE007VJ17"
                                                         CTCTCCCTGTCTCCGGGTAAATGA 731
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HTC; CNSLT CDNA.
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end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1. 1090

/organism="Hono sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSODIO71YG21"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pcMVSpORT_6"
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Pred. No. 1.4e-178;
0; Mismatches 1;
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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1 (bases 1 to 1090)
1 ("I, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                                                         TTCCTCTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
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Placenta Cot
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1093 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI048YC07 of Placenta Cot 25-normalized of 4non sapiens (human).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="mRNA"
/db_xref="teaxon:9606"
/clone="CSODIO48XC07"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Homo sapiens
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191 91006 BVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
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/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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     CR604961.1 GI:50485768
HTC; CNSLT_CDNA.
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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Score 682.4; DB 3;
Pred. No. 1.4e-178;
0; Mismatches 1;
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   Query Match
Best Local Similarity 99.9%;
Matches 683; Conservative
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoN V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitogen.
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Catarrhini; Hominidae; Homo.
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full-length cDNA clone CSOCAP001YII3 of Thymus of Homo sapiens
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Mammalia; Eutheria; Primates; Catarrhini; Hoo
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1. W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSOCAPOOIYII3"
/tissue_type="Thymus"
/plasmid="pCMVSPORT_6"
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HTC; CNSLT_CDNA.
HOMO SADIENS (human)
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Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                           HTC 21-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 TGCGTGGTGGTGGACCTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTTGGTACGTGGAC 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 GACAAAACTCACCATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGCCGTCAGTC 378
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Catarrhini; Hominidae; Homo.
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full-length cDNA clone CSOCAP008YF07 of Thymus of Homo sapiens
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                                                                                                                                                                                                                                                                                                                            Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Mammalia; Eutheria; Primates; Catarrhini; Hon
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1. (bases 1 to 1102)
Full-length cDNA libraries and normalization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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HTC; CNSLT CDNA.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoP V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

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Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
Full-length, CDNA libraries and normalization
                                                                      743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
                                                                                                                                                   CGTGTGGTCGTCGTCCTCCCCGTCCTGCACCAGGCTGATGGCAATGGCAAGGAGTACAGG
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoN v sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                     1293
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                                                                      TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                       AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
                                                                                                                                                   GACGGCTCCTTCTTCCTCTACAGCTCACGTGGACAAGAGAGCAGGTGGCAGCAGGAGCAGGGG
                                                                                                   799 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue 2 (bases 1 to 1102)
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/clone="CSDIO59YL06"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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                                                            Query Match 49.6%; Score 682.4; DB 3; Best Local Similarity 99.9%; Pred. No. 1.4e-178; Matches 683; Conservative 0; Mismatches 1;
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/clone="CSODE010YH13"
/tissue_type="placente"
/plasmid="pcMvSpORT_6"
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/RegCOMB.seq:*
/cgn2_6/ptodata/1/ina/RegCoMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Patent No. 6833349
GENERAL INFORMATION
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT PILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SSQ ID NO 25
LENGTH: 1377
                                                                                  Sequence Seq
   Sequence
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                        US-08-487-550-7

US-09-526-098-7

US-08-133-916-7

US-08-130-175-7

US-08-130-175-7

US-08-130-175-7

US-09-499-846-5

US-09-499-846-3

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US-09-133-94-52
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100.0%; Score 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches
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          APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 1453
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                                                                                                                                                TYPE: DNA
ORCANISM: Artificial Sequence
FEATURE:
THER INFORMATION: F1L1D2.F1k1D3.FcdeltaC1(a)Receptor
NAME/KEY: CDS
1.0CATION: (69)...(1442)
US-09-773-877B-21
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 GENERAL INFORMATION:
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Squence 23, Application US/09773877B
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86.7%; Pred. No. 6.7e-271;
tive 0; Mismatches 158; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 86.7
Matches 1201; Conservative
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US-09-773-877B-23
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                     TCTGTTGGAGAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTGAAATGTGGGGATT
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                                                                                                                                              TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1311
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CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1190
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                              TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAAGCAATGGGCAG
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Sequence 15, Application US/09773877B

Fatent No. 6813349

GENERAL INFORMATION:

APPLICANT: Xia, Yu-Ping et al.

TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

FILE REFERENCE: REG 710b

CURRENT APPLICATION NUMBER: US/09/773,877B

CURRENT PILING DATE: 2001-01-31

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 15
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86.3%; Pred. No. 3.5e-268;
live 0; Mismatches 170;
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US-09-773-877B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 1189; Conservative
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                                                766 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGGACCCCTGAGGTCACA
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                        TTCCTCTTCCCCCCAAAACCCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT PILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOSTWARE: Patentin version 3.0
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B6.1%; Pred. No. 2.6e-254;
tive 0; Mismatches 171;
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OTHER INFORMATION: Flt1(1-3 deltaB) (Mut 1)
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Best Local Similarity 86.1;
Matches 1119; Conservative
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US-09-773-877B-13
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US-09-773-877B-13
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706 GACAAAACTCACACACTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTC 765
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      APPLICANT: Xia, Yu-Ping et al.

TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
LENGTH: 1389
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                                                                                                                                                                                                                                                                                                                                                                                   Length 1389;
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75.0%; Score 1032.4; DB 4; Length
Best Local Similarity 85.5%; Pred. No. 2.1e-266;
Matches 1201; Conservative 0; Mismatches 161; Indels
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                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (1)..(1389)
US-09-773-8778-17
GENERAL INFORMATION
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                                                                                                                                        AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1635
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Patent No. 6833349
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT PLING DATE: 2010.01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 1704
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Pred. No. 5.7e-253;
0; Mismatches 161;
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ilarity 85.4%;
Conservative 0
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ORGANISM: Artificial Sequence
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Matches 1132; Conserv
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US-09-773-877B-19
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US-09-773-877B-19
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Flt1(1-3)-FC
NAME/KEY: CDS
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Best Local Similarity 85.3
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Patent No. 683349
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
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J. T. Line Spine J. D.

.039 ccaccereccaecaccreaacrecreeeeeaaccercaercrerecrerecceccaaaa 1098 cccaaggacacccrcargarcrcccgaccccrcaggrcacargcgrgcrcgrcgrcgrc 1158 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAAT 1218 138 378 678 978 771 198 258 318 438 618 918 831 891 951 444 504 564 624 684 GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC 498 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGG 558 828 685 Arcaradargrecaaaraageacaecaeceeegreaaarracrragaggeearaerir 744 745 GTCCTCAATTGTACTGCTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804 CCT-----GATGAAAAAATAAGAGAGCTTCCGTAAGGCGACGAATTGACCAAAGCAAT GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC GGACTTTATACTTGTCGTGTAAGGAGTGGACCATCATTCAAATCTGTTAACACCTCAGTG AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCCGAAATTATACACATG ACTGAAGGAAGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT TTAAAAAAGGTTTCCACTTGACACTTTGATGCCTGATGGAAAACGCATAATCTGGGACAGT AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCCTTCTGACCTGTGAA CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA TTAAAAAACGTTTCCACTTGACCTTGATCCCTGATGGAAAACGCATAATCTGGGAACGT AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATGGACAAACCAATACA CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGTGGTG GCCAAGACACACGCGCGCAGGAGCAGTACAA CAGCACGTACCGTGTGGTCAGCGTCTC ACTGAAGGAAGCGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT ATCATAGATGTGGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT 559 AGTGAGATGAAGAATTTTTGAGCACCTTAACTATAGATGGTGTAACCCGGAGTGACCAA AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAAT Gaps 33; Length 1704; Indels Score 980.8; DB 4; Pred. No. 1.5e-252; 0; Mismatches 162;

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1730 GAGAACCACAGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACAGGTCA 1789
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                                                                                                                                                                                                                                            NAME/KEY: tICAM(453)/IgG fusion
OTHER INFORMATION: bp 1-1359 = nucleotides coding
OTHER INFORMATION: for amino acid residues 1-453 of ICAM-1; bp 1360-
OTHER INFORMATION: 2040 = nucleotides coding for amino acid residues
OTHER INFORMATION: 216-442 of human heavy chain IgG1; bp 2401-2043 =
OTHER INFORMATION: stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1430 CCCCAAAACCCAAAGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                             49.8%; Score 686; DB 3; Length 20
95.9%; Pred. No. 1.6e-173;
ive 0; Mismatches 30; Indels
                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: other nucleic HYPOTHETICAL: no
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TELEFAX: (203) 812-5492
INPORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2043 Dp
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.9
Matches 704; Conservative
                                                                 LENGTH: 2043 bp
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                ANTI-SENSE: no
FEATURE:
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                                                                                                                                    GCCCTCCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA
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                  ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
                                                                                                                                                                                                CAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC
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                                                                                                          GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCCAAAGGGCAGCCCCGAGAACCA
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US-08-27-496C-14
; Sequence 14, Application US/08227496C
; Patent No. 6130202
; GENERAL INPORMATION:
APPLICANT: Greve, Jeffrey M. APPLICANT: McClelland, Alan
; TITLE OF INVENTION: Multimeric Forms of Human
; TITLE OF INVENTION: Rhinovirus Receptor Protein
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP.
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COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 1.44 Mb storage COMPUTER: Dell Optiplex GXI
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect 8.0 for Windows SOFTWARE: Wordberfect 8.0 for Windows APPLICATION NUMBER: US/08/227,496C
FILING DATE: 04/14/94
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/903,069
FILING DATE: 06/22/92
APPLICATION NUMBER: 07/904,984
FILING DATE: 06/22/92
APPLICATION NUMBER: 07/56,238
FILING DATE: 07/20/90
ATTORNEY AGENT INFORMATION:
NAME: Barbara A. Shimei
REGESTRATION NUMBER: 29,862
REFERENCE/DOCKET NUMBER: MTI 214.2C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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1174 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1233
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                                                                                                       305 TGCAAGGTCTCCAACAAAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGGCCAAA 364
                                                                                                                                                                                                              365 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 424
                                                                                                                                                                                                                                                                                                             425 AACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTATCCCAGCGACATCGCGGGGA 484
245 CGTGTCGTCACCTCCACCGTCCTCCACCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       545 GACGGCTCCTTCTTCTTCTACAGCAAGCTCACGTGGACAAGAGCAGGTGGCAGCAGGGG 604
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Sequence 1, Application US/09178869B

Sequence 1, Application US/09178869B

GENERAL INFORMATION:
APPLICANT: Tao, Weng

APPLICANT: Hackey, William F

APPLICANT: Hammang, Joseph P.
APPLICANT: Baetge, E. Edward

TITLE OF INVERTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REPERENCE: 17810-043

CURRENT APPLICATION NUMBER: US/09/178,869B

CURRENT FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 14

SOFTMARE: PATENTIN Ver. 2.0
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NAME/KEY: gene
LOCATION: ()...)
OTHER INFORMATION: Polynucleotide
FEATURE:
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; LOCATION: (16)..(1008)
US-09-178-869-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFFWAIRS: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
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Pred. No. 3.4e-173;
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100.0%; Pred. No. 5...
0; Mismatches
                                                                                                            Sequence 1223, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
APPLICANT: Cocke, Benjamin G.
APPLICANT: Guern G. Stuart
APPLICANT: OFFICEY J. Sellhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1223:
SEQUENCE CHARACTERISTICS:
  2030 CTCCGGGTAAATGA 2043
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TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: PALO ALTO STATE: CALIFORNIA
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; CLONE: 9243865
US-09-023-655-1223
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Best Local Similarity
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                                                                                                 US-09-023-655-1223
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APPLICANT: Tao, Weng
APPLICANT: Tao, Weng
APPLICANT: Wong, Shou
APPLICANT: Hammang, Joseph P.
APPLICANT: Hammang, Joseph P.
APPLICANT: Bactege, B. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/178,869
PRIOR APPLICATION NUMBER: US/09/178,869
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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| NAME/KEY: gene | LOCATION: ()...) | OTHER INFORMATION: Description of Sequence: Recombinant | OTHER INFORMATION: Polynucleotide | NAME/KEY: CDS | LOCATION: (16)..(1008) | US-09-761-413-1
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Patent No. 6506891
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US-09-761-413-1
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      Length 1019;
                                                             Indels
   49.7%; Score 684; DB 4; L. 100.0%; Pred. No. 4e-173; ive 0; Mismatches 0;
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APPLICANT: NAKAMURA, No. 6306395io
APPLICANT: NAKAMURA, Shigekazu
ITILB OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P;
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER APPLICATION NUMBER: PCT/JP97/01502
SAFLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 18
LENGTH: 1182
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Query Match
Best Local Similarity 100.
Matches 684; Conservative
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CORGANISM: Homo sapiens
US-09-180-100-18
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985 CGTGTGGTCCTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGAGAGTACAAG 1044
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                                                                                      MCRUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,376
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPHORE: (703) 836-620
TELEPHORE: (703) 836-620
TELEPHORE: (703) 836-620
SECURATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
49.7%; Score 684; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 4.6e-173;
Matches 684; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                             Floppy disk
                  United States
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..1428
                     COUNTRY: United ZIP: 22313-1404
Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-488-376-19
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Sequence 19, Application US/08488376

GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
APPLICANT: PAN, Li-Zhen
APPLICANT: PAN, Li-Zhen
APPLICANT: NEWAMAT, Soulaima Anthony
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Roland Anthony
APPLICANT: HEARD, NEWAMAN Roland Anthony
TITLE OF INVENTION: MUNOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Burna, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
CITY: Alexandria
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                                                                                                                       TTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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                     Length 1182;
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              49.7%; Score 684; DB 3; Le
100.0%; Pred. No. 4.2e-173;
ive 0; Mismatches 0;
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                                                        684; Conservative
                                   Similarity
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US-08-488-376-19
              Query Match
Best Local S
Matches 684
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Search completed: S
Job time : 275 secs
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                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/08634223
Patent No. 5840298
GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
APPLICANT: CHANAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: WALSH, Edward E.
APPLICANT: WALSH, Soland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                             1285 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGG 1344
                                                   754 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
STATE: Virginia
COMPUTRY: United States
ZIP: 2313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/488,376
FILING DATE: 07-JUN-1995
ATTONNEY/AGENT INPORMATION:
ANAME: GALLING DATE: DATHER OF ALLING DATE: DATHER DATE: DATE: DATHER DATE: DA
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Best Local Similarity 100.0%; Pred. No. 4.6e-173;
Matches 684; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Burns, Doane, Swecker & Mathis P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALICKNEI, TOCKNEI, THE CANALLIANA

NAME: TERKIN, RODIN L.

RECISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-150

TELEPHONE: (703) 836-620

TELEPAX: (703) 836-2021

INFORMATION FOR SEC ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs

TYPE: nucleic acid

STRANDENNESS: single
                                                                                                                                                      CICTCCCTGTCTCCGGGTAAATGA 1377
                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..1428
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LOCATION:
US-08-634-223-19
                                                                                                                                                                                                                                                                                    RESULT 15
US-08-634-223-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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Sequence

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TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
Query Match
Best Local Similarity
Matches 1377; Conserv
US-09-773-877A-25
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US-10-860-958-1
US-10-830-902-1
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US-10-909-011-3
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Maximum Match 100%
Listing first 45 summaries
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
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US-10-988-243-15
US-10-998-881-3
US-11-016-097-15
US-10-998-881-3
US-10-999-875-77
US-10-999-881-1
US-10-999-881-1
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Publication No. US20040014667A1;
GENERAL INFORMATION:
APPLICANT: Thomas D. Fand;
APPLICANT: Thomas D. Fand;
APPLICANT: Thomas D. Fand;
APPLICANT: Thomas D. Fand;
APPLICANT: Nicholas J. Papadopoulos
ITILE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
FILE REFERENCE: REG 710D
CURRENT APPLICATION NUMBER: US/10/609,775
CURRENT APPLICATION NUMBER: PCT/US00/14142
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASELED for Windows Version 4.0
SEQ ID NOS: 25
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; ORGANISM: homo sapiens
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APPLICANT: Yamashiro, Darrell
APPLICANT: Huang, Jianzhong
APPLICANT: Huang, Jianzhong
APPLICANT: Yancopoulos, George
APPLICANT: Rudge, John
TITLE OF INVENTION: Inhibitors
TITLE OF INVENTION: Inhibitors
TITLE OF INVENTION: Inhibitors
FILE REPERENCE: REG 714A
CURRENT APPLICATION NUMBER: US/10/860,958
CURRENT FILING DATE: 2004-06-04
PRIOR PELICATION NUMBER: 60/476,425
PRIOR FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1277
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CRGANISM: homo sapiens
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Sequence 1, Application US/10860958 Publication No. US20040265309A1 GENERAL INFORMATION: APPLICANT: Kandel, Jessica APPLICANT: Holash, Jocelyn

RESULT 3 US-10-860-958-1 721

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APPLICANT: Stanley Wiegand

APPLICANT: Claus Cursiefien

TITLE OF INVENTION: Method of Treating Corneal Transplant

TITLE OF INVENTION: Rejection

FILE REFERENCE: REG 713B

CURRENT APPLICATION NUMBER: US/10/830,902

CURRENT FILING DATE: 2004-04-23

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FRAESEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: homo sapiens
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Sequence 3, Application US/10909011
; Sequence 3, Application US/10909011
; Publication No. US20050112061A1
; GENERAL INFORMATION:
; APPLICANT: George Yancopoulos
; APPLICANT: George Yancopoulos
; APPLICANT: Application With Radiation Therapy
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
; FILE REFERENCE: REG 716A
; CURRENT APPLICATION NUMBER: US/10/909,011
; CURRENT FILING DATE: 2004-07-30
; PRIOR PLING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FRAESEQ for Windows Version 4.0
; TENGEN TO NOS: 4
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CRGANISM: homo sapiens
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CURRENT FILING DATE: 2004-06-29
FRIOR APPLICATION NUMBER: 10/609,775
FRIOR FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 29
SECTIANGE FREUSEQ for Windows Version 4.00
EDSTGARES FREUSED FOR WINDOWS VERSION 4.00
TYPE: DNA
TYPE: DNA
US-10-880-021-9
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g 8	241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATCAAATGCAACGTACAAGAAATA 300	Db 1321 GAGGCTCTGCACACACACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGTAAATGA 1377
& 8	301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360 	RESULT 8 US-10-988-243-15 ; Sequence 15, Application US/10988243
දු පු	361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420 	ው ወ
දු පු	421 TCTGTTGGAGAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480 	; APPLICANT: Yancopoulos, George ; TITLE OF INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinectic Pro ; TITLE OF INVENTION: and Methods of Making and Using Thereof ; FILE REFERENCE: REG 710F
දු පු	481 GACTICAACIGGGAATACCCTICTICGAAGCAICAGCATAAGAAACIIGIAAACCGAGAC 540 	CURREN CURREN PRIOR PRIOR
දු දු	541 CTAAAAACCCAGTCTGGGAGTGAGAAGAAATTTTTGAGCACCTTAACTATAGATGGT 600 	; PRIOR APPLICATION NUMBER: PCT/USOO/14142 ; PRIOR FILING DATE: 2000-05-23 ; PRIOR APPLICATION NUMBER: 60/138,133 ; PRIOR FILING DATE: 1999-06-08
ço q	601 GTAACCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660 	
<u>ک</u> ۾	661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACATGCCCACGTGC 720 :	; TYPE: DNA ; ORGANISM: Homo sapiens US-10-988-243-15
<u>ک</u> و	CCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ර සි	ACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCACGAAAACCTCATGAGCCTCGAGCCTCGAGCACGAAAACCTCACTGAGCCTCGAGCCTCGAGCAACGAAAAACCTCATGATGATGAGCTCAAAAAAAA	Oy 1 AIGGTCAGCTACTGGGACACCGGGGGTCCTGCTGTGCTCCAGCTGCTTCTC 60
\$ & B	GACCCTGAGGTCAAGTTCAACTGGTACGACGGCGTGGAGGGTGCATAATGCCAAGACA 	Oy 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120
B & B	AGCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Oy 121 CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
y d	CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCCAACAAAGCCCTCCCAACAGAACTGCAAGAAGTCTCCAAGAAGTGCAAGGTACAAGGTCTCCAAGAAGTGCAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTCCAAAGGTCTTCCAAAGGTCAAGGTCTTCCAAAGGTCTTCTTCCAAAGGTCTTCTTCTTTCT	Oy 181 CCTAACATCACTGTTACAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA 240 Db 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCTGATGGAAAA 240
<u>ک</u> و		Oy 241 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA 300
ò q	ACCCTGCCCCCATCCCGGGATGAGCTGACCAGGTCAGCCTGACCTGCCTG	Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
ර සි		Oy 361 CATGACAAACCAATACAATGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420
ò q	1 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTTCTTCTACAAGCAAG	Oy 421 TCTGTTGGAGAAAGCTTGTCTTAAATTGTACAGAACTGAACTAAATGTGGGGGATT 480

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100.0%; Score 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/998,881
CURRENT FILING DATE: 2004-11-29
FRIOR APPLICATION NUMBER: 10/909,011
PRIOR FILING DATE: 2004-07-30
FRIOR FILING DATE: 2004-07-30
FRIOR FILING DATE: 2000-08-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1377
                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: homo sapiens
US-10-998-881-3
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Publication No. US20050196340A1
GENERAL INFORMATION:
APPLICANT: Jocelyn Holash
APPLICANT: George Yanocpoulos
APPLICANT: Adam P. Dicker
APPLICANT: Adam P. Dicker
APPLICANT: Randy Burd
TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
FILE REFERENCE: 716B
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| Publication No. US20050163798A1
| GENERAL INFORMATION:
| APPLICANT: Nicholas J. Papadopoulos et al.
| APPLICANT: Nicholas J. Papadopoulos et al.
| TITLE OF INVENTION: MODIFIED CHIMMERIC POLYPEPTIDES WITH IMPROVED
| TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
| TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
| TITLE OF INVENTION: ADDU USING THEREOF
| TITLE OF INVENTION: ADDU USING THEREOF
| FILE REFERENCE: REG 710-A-US
| CURRENT FILING DATE: 2004-12-17
| PRIOR APPLICATION NUMBER: US/10/009,852
| PRIOR FILING DATE: 2000-05-23
| PRIOR FILING DATE: 2000-05-23
| PRIOR FILING DATE: 1999-06-08
| NUMBER OF SEQ ID NOS: 38
| SEQ ID NO 15
| LENGTH: 1377
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ORGANISM: Homo sapiens
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GENERAL INFORMATION: APPLICANT: Xia, Yu-Ping et al.
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Publication No. US20050197291A1

GENERAL INFORMATION:
APPLICANT: Stanley Wiegand
APPLICANT: Jingtai Cao
ITILE OF INVENTION: Method of Treating Corneal Transplant
ITILE OF INVENTION: Rejection In High Risk Keratoplasty Patients
FILE REPERENCE: 713C
CURRENT APPLICATION NUMBER: US/11/039,144

CURRENT PILING DATE: 2005-01-19
FRIOR PILING DATE: 2004-04-203
FRIOR APPLICATION NUMBER: 60/473,734
FRIOR PILING DATE: 2003-05-28

NUMBER FO SEQ ID NOS: 2

SEQ ID NOS: 2

SEQ ID NO 1

SEQ ID NO 1
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 1377; Conservative
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| Sequence 7, Application US/10609775
| Publication No. US20040014667A1
| GENERAL INFORMATION:
| APPLICANT: Thomas J. Daly
| APPLICANT: Thomas P. Fandl
| APPLICANT: Oames P. Fandl
| APPLICANT: Micholas J. Papadopoulos
| TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
| TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
| TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
| TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
| TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
| TITLE OF INVENTION NUMBER: 10/009,852
| PRIOR APPLICATION NUMBER: 10/009,852
| PRIOR APPLICATION NUMBER: 60/138,133
| PRIOR APPLICATION NUMBER: 60/138,133
| PRIOR FILING DATE: 2000-06-23
| WINDRER OF SEQ ID NOS: 25
| VEGFTANER: FASTSEQ for Windows Version 4.0
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Best Local Similarity 98.6%;
Matches 1367; Conservative
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                         Length 1453;
                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                                                    OTHER INFORMATION: Flt1D2.Flk1D3.FcdeltaC1(a)Receptor
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Pred. No. 0;
0; Mismatches
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                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (69)..(1442)
US-09-773-877A-21
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Best Local Similarity
Matches 1367; Conservat
                                                                                                                      LENGTH: 1453
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APPLICANT: Jocelyn Holash
APPLICANT: George Yancopoulos
APPLICANT: George Yancopoulos
APPLICANT: Adam P. Dicker
APPLICANT: Adam P. Dicker
APPLICANT: Randy Burd
TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
FILE REPERBNCE: REG 716A
CURRENT APPLICATION NUMBER: US/10/909,011
PRIOR APPLICATION NUMBER: 60/492,864
PRIOR FILING DATE: 2003-08-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0;
0; Mismatches
                                   Sequence 1. Application US/10909011; Publication No. US20050112061A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.6%;
Matches 1367; Conservative 0
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Search completed: September 23, 2005, 17:12:40 Job time : 937 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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SWART; SM00409; IG; 3.
SWART; SM00409; IGC1; 2.
SWART; SM00406; IGC2; 2.
SWART; SM00406; IGV; 2.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS002200; IG MHC; UNKNOWN 1.
SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 TYKEIGLLTCEATVNGHLYKTNYLTHRO---TNTIIDV-------VLSPSHGIELS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 VGEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 SGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVL-----QSSGLYSLSSVVTV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 PSSSLGTQ-TYICNVNH----KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLF 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 PPKPKDTLMISKTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSKDELTKNQV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLITCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLIVDKSRWQQGNVF 434
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                                                                                                                                                                                                                                                                                                                                                            59 T----SPNITVTLKKFPLDTLIPDGKRIIW------DSRKG-FIIS----NA 95
                                                                                                                                                                                                                                                                     ::|:||:||:|
1 MEFWLSWVFLVAILKGVQCEVQLVESGGG-------LIQPGGSLTLSCAA
                                                                                                                                                                                                                                                                                                                                                                                                               44 SGLTVSSNYMHWVRQAP-----GKGLEWVSVLYIGGATYYADSVKGRFTISRDNSKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
                                                                                                                                                                                                                                2 VSYWDTGVLLCALL---SCLLLTGSSSGSDTGRPFVEMYSEIPEIHMTEGRELVIPCRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 DGVTRSDQGLYTCAASSGLMTKKNSTFV--RVHEK--DKTHTCPPCPAPELLGGPSVFLF
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A Qi Y., Xiang J.;
A Qi Y., Xiang J.;
I.A genetically engineered single-gene-encoded anti-TAG72 chimeric artibody secreted from myeloma cells.";
I. Hum. Antibodies Hybridomas 6:161-166(1995).
E EMBL, 882493; AAB87424.2; -..
R INTERPO: IPR001599; Ig.
R INTERPO: IPR001599; Ig.
R INTERPO: IPR001599; Ig.
R INTERPO: IPR001506; Ig.
R INTERPO: IPR001506; Ig.
R INTERPO: IPR001506; Ig.
R INTERPO: IPR001506; Ig.
R PF007654; Cl-set; Z.
R Pfam; PF007654; Cl-set; Z.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10095,
                                                                                                                                                                       85;
                                                                                             Query Match 52.0%; Score 1267.5; DB 2; Length 466; Best Local Similarity 55.8%; Pred. No. 8.3e-80; Matches 281; Conservative 34; Mismatches 104; Indels 85;
PS00290; IG MHC; UNKNOWN 2.
466 AA; 50853 MW; 53EB0BCEDE81076E CRC64;
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Last annotation update)
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   PROSITE;
SEQUENCE
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AC 065Z-0
DT 25-0
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                                                                                                                                                                                                                                      SPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLV------NRD 180
                                                                                                                                                                                                                                                                   295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
                                                                                                                                                                                                                                                                                                                                                181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGL-MTKKNSTFVRVHEK----DKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 HNAKTKPREEQYNSTYRVFSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
                                                                Gaps
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A wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

R Fobo G., Han M., Wiemann S.;

L Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640627; CAE45781.1; -..

R HSSP; P01861; 1ADQ.

R InterPro; IPR003599; Ig.

R InterPro; IPR003597; Ig.C1.

R InterPro; IPR003597; Ig.C1.

R InterPro; IPR003597; Ig.C1.

R InterPro; IPR003597; Ig.C1.

R START; SM00409; IG; 2.

SWART; SM00409; IG; 2.

R SMART; SM00406; IGV; 1.

R PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Query Match 51.4%; Score 1253.5; DB 2; Length 487; Best Local Similarity 64.5%; Pred. No. 8.2e-79; Matches 260; Conservative 29; Mismatches 67; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686FP15220.
Name=DKFZp686FP15220;
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Best Local Similarity 62.43
Matches 262; Conservative
                                                                                                                                                          InterPro, IPR003599, Ig.
                                                                        SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
    Jones S.J., Marra M.A.;
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SEQUENCE FROM N.A.
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WEDLINE-ETHMATY B-Cells;

WEDLINE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Habteh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.I., Scheetz T.E.,

A Stapleton M., Goares M.B., Donaldo M.F., Casavant T.I., Scheetz T.E.,

A Roberstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

A Richards S., Worley M.M., Sodergren E.J., Lu X., Gibbs R.A.,

Willalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Willialon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RKIZywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                           ----QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNH-----KPSNTKVDKRVEPKSCDKTHT 250
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                                                                                                                                                                         G-FIIS-----NATYKEIGLLTCEATV------NGHLYKTNYLTHRQTNTIIDV- 130
                                                                                                                                                                                         131 -----VLSPSHGIELSVGEKLVINCTARTELNVGIDFNWE---YPSSKHQHKKLVNRD 180
                                                                                                                                                                                                                                                   CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 296
                                                                                                                                                                                                                                                                                                                                                                                                             NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 356
                                                                                                                                                                                                                                                                                                                                                                                                                            PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 430
                                                                                                                  88
                                                                                                                                            34 GRSLRLSCAASG-----FTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAYADSVK 84
                                                                                                                                                                                                                                                                                          181 LKTQSGSEMKKFLSTLT1DGVTRSDQGLYTCAASSGLMTKKNSTFV--RVHEK--DKTHT
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                    75;
                                                          DB 2; Length 472;
                                                      Query Match 51.4%; Score 1252.5; DB 2; Length Best Local Similarity 59.1%; Pred. No. 9.3e-79; Matches 273; Conservative 24; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                l protein.
472 AA; 51724 MW; 26CB340D0046D279 CRC64;
                                                                                                                 GRELVIPCRVTSPNITVTLKKFPLDTLI-----PDGKRIIW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
PS00290; IG_MHC; UNKNOWN_2.
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05-JUL-2004 (TrEMBLrel. 27, Cx
05-JUL-2004 (TrEMBLrel. 27, La
05-JUL-2004 (TrEMBLrel. 27, La
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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             Hypothetical
SEQUENCE 47
                                                                                                                                                                                                                                                                                                                       200
 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 GKRIIW------DSRKG-FIIS----NATYKEIGLLTCEATV-----NGH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 LYKTNYLTHRQTNTIIDV------VLSPSHGIELSVGEKLVLNCTARTELNVGID 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
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              full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 FNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 VSWNSGALISGVHTPPAVL-----QSSGLYSLSSVVTVPSSSLGTQ-TXICNVNHKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQQNVFSCSVWHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 TKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 470;
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IFRO03597; 19-1ike.
InterPro; IFRO03597; 1g-1ike.
InterPro; IPRO03597; 1g-1ike.
InterPro; IPRO03506; 1g-W.
InterPro; IPRO03506; 1g-W.
InterPro; IPRO03506; 1g-W.
InterPro; IPRO0409; 1G, 2.
SWART; SW00400; 1G0, 2.
SWART; SW00406; 1GV, 1.
IPROSITE; PS00290; 1G-MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                  Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
EMBL, BCO18747; AAH18747.1; -.
HSSP; P01861; 1ADQ.
"Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheital protein DKFZp686G11190.
Name=DKFZp686G11190,
                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.4%; Score 1252; DB 2; 162.4%; Pred. No. 1e-78;
tive 23; Mismatches 85;
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Astraubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.T., Zeeberg B. Buetow K.H., Schaefer C.F., Blate N.K.,

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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haidh F.,

Astapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rack S.A., McZwan P.J., McKernan R.J., Malek J.A., Gunarate P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rack S.A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rackiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Geberzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 EVICVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ATVNGHLY------KTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 FPERVIVSWNSGALTSGVHTFPAVL-----QSSGLYSLSSVVTVPSSSLGTQ-TYICN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 LNVGIDFNWE----YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSGLMTKKNSTFV--RVHEK--DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 GKRIIW-----DSRKG-FIIS----NATYKEIGLLTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478 AA; 52666 MW; 17BED38D917970D6 CRC64;
                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.1%; Score 1246; DB 2;
61.6%; Pred. No. 2.7e-78;
ive 23; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR00710; Ig-c1.
InterPro; IPR003596; Ig-wHC.
InterPro; IPR003596; Ig-wHC.
InterPro; IPR004596; Ig-wHC.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                       BC041037; AAH41037.1;
P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                       cDNA sequences.
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les 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           IISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein
SEQUENCE 478 AA;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       and mouse
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HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 KPSNIKVDKKVEPKSCDKIHICPPCPAPELLGGPSVFLFPPKPKDTLMISRIPEVICVVV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLS 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTHRQT-----NTIIDVVLSPSHGIEL-----SVGEKLVLNCTARTELNV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 PVTVSWNSGALTSGVHTFPAVL------OSSGLYSLSSVVTVPSSSLGTQ-TYICNVNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDYQVSPAYWYFDVWGRGTLVSVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIDFNWE---YPSSKHOHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                    Fobo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                          51;
                                   Α.,
                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 475;
          The German Human Consortium;
The German Human Consortium;
The German Human Consortium;
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A.,
Han M., Wiemann S.;
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A.,
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A.,
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A.,
E. Shahited (Aug-203) to the EMBL/GenBank/DDBJ databases.
R HSSP, PO1861, 1ADO.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R SMART; SMO0406; Ig. 2.
SMART; SMO0407; IGC. 1.
R SMART; SMO0407; IGC. 1.
R R SMART; SMO0407; IGC. 1.
R R SMART; SMO0407; IGC. 1.
R PROSITE; PSOS0835; IG. LIKE; 4.
R PROSITE; PSOS0835; IG. LIKE; 4.
R PROSITE; PSOS0835; IG. LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                          88; Indels
                                                                                                                                                                                                                                                                                                      .l protein.
475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     51.1%; Score 1246.5; DB 361.0%; Pred. No. 2.4e-78; ive 26; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
   TISSUE=Human esophagus tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27,
27,
27,
                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 61.0
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel. Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                           GKRIIW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGK 458
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                                                                                                                                                                                                                                                                                                         Hypothetical
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268 288 328 468

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mouse cDNA sequences."
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                                                                                                                282
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Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Milahy S.J.,

Raha S.S., Morley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krywinski M.I., Skalsku U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human and mouse colly a sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 PDGKRIIWDSR----KGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQT----- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------NTIIDV-----VLSPSHGIELSVGEKLVLNCTARTELNVGIDFNW 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 51.1%; Score 1245.5; DB 2; Length 465; al Similarity 61.9%; Pred. No. 2.8e-78; 258; Conservative 23; Mismatches 91; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC073766; AA473766.1; -.
R InterPro; IPR007110; Ig-1ike.
R InterPro; IPR003595; Ig c1.
R InterPro; IPR003596; Ig wHC.
R InterPro; IPR003596; Ig wHC.
R InterPro; IPR003596; Ig wHC.
R Ffam; PF07654; C1-set; 3.
R SMART; SM00407; IG; 1.
R SMART; SM00409; IG; 1.
R SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                      PRT;
                                                                                                             (TrEMBLrel. 27, C
(TrEMBLrel. 27, L
(TrEMBLrel. 27, L
                                                                                      PRELIMINARY;
                       469 OKSLSLSPCK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE=Primary B-Cells;
                                                                                                                                                 Hypothetical protein
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein
449 QKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                               05-JUL-2004
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Astraubberg R.L., Feingold E.A., Grouse L.H., Derge JG.

Astraubberg R.L., Feingold E.A., Grouse L.H., Derge JG.

Astraubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Astrachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Astrachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Astrachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Astrachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Wokin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,

Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

Raber J., Helton B.K. Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butteerfield Y.S.,

And Mullishial and Initial analysis of more than 15,000 full-length human

T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 408
119 FTYFDYWGQGTLVTVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLVKDYFPEPVTVSW 176
                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 401
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                                                                                                                                                                                                                                                                                                                                                     229 VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPRPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                            177 NSGALTSGVHTFPAVL-----QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNHKPSNTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
                                                                                                165 E---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKK
                                                                                                                                                                                                                                                                                             222 NSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (UTM-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BCO13773; AAH73773.1; -.
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR00478; Ig.
InterPro; IPR00479; Ig. 4.
SWART; SW00409; IG; 2.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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482
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PROSITE; PS00290; IG MHC; UNKNOWN_2.
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                                                                                                                                                                                                     InterPro; IPR003597; Ig. 11.
InterPro; IPR003597; Ig. 11.
InterPro; IPR003596; Ig. WHC.
InterPro; IPR003596; Ig. V.
Pfam; PF00447; Ig. 4.
SMART; SM00407; IG; 2.
SMART; SM00406; IGC1; 1.
                                                                   and mouse cDNA sequences.
Proc. Natl. Acad. Sci. U.
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                                                                                                            SEQUENCE FROM N.A.
TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                             Hypothetical
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118 RAGVWGSFRSWAIDGFNIWGQGTWVTVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLV 175
                                                                                                                                                                                                                                                              209
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                                                                                                                                                                                                                                                                                                                                  228 ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE 287
                                                                                                                                                                                                                                                                                                                                                                                                 347
                                                                                                                                                                                                                                                                                                                                                                                                                          YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                          YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQ 467
                                                                                                                                                                                                                                                                            VICOVVDOSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                    61 PPGKGLEW---IGYIYYSGSTYYNPSLKSRVTISLDTSRNQFSLKMNSVTAADTAVYFCA
                                                                                                                                                                                                       ------VLSPSHGIELSVGEKLVLNCTA
                                                                                                                                                                                                                                                                                                                                                                      VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                                                                                                                                                                             RTELNVGIDFNWE----YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLY
                                                                                                                                                                                                                                                                                                                 TCAASSGLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Straubberg R. L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                   77 PDGKRIIWDSRKGFI-ISNATYKEIGL----LTCEATVNGHLYKTNYLTHRQT----
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                 Length 476;
                                                                                                                          85; Indels
                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                              51.1%; Score 1245; DB 2;
60.8%; Pred. No. 3.1e-78;
ive 23; Mismatches 85;
                                                     Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABASC62DDE9D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               475
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                       261; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel.
Hypothetical protein.
Homo sapiens (Human).
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                     Strausberg R.; Strausberg R.; Strausberg R.; Submitted (dUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC073782. AAH73782.1; -. InterPro; IPR001599; IG. InterPro; IPR007110; IG-like.
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686N02209.
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Ellison J.W., Berson B.J., Hood L.E.; "The nucleotide sequence of a human imm Nucleic Acids Res. 10:4071-4079(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BONDS.
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   -------PSSSKHQ 172
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                               TISSUE=Human rectum tumor;
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Subbaitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX38118; CAD98026.1; -.
HSSP; P01857; 11ZH.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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57.1%; Pred. No. 4.7e-78;
ive 27; Mismatches 100; Indels
                                                                                                                                                                                                                                                                            GRELVIPCRVT----SPNITVTLKKFPLDTLIPDGKRIIW-----
                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
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PROSITE; PS00290; IG MHC; UNKNOWN_2.
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                                                                                               IndexPro; IPR007110; Ig-like.
IntexPro; IPR003597; Ig_cl.
IntexPro; IPR003065; Ig_MHC.
IntexPro; IPR003596; Ig_V.
Pfam; PF07654; Cl-set; Ig_V.
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SMART; SM00406; IGv; 1.
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Name=IGHG1;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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"The rule of antibody structure. The primary structure of a monoclonal
IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
peptides of the H-chain, alignment of the tryptic peptides and
discussion of the complete structure.",
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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immunoglobulin C gammal gene.";
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MEDLINE=83289131; PubMed=6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
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-!- MISCELLANEOUS: Nie also differs in the amidation states of 35, 116, 198, 269 and 272.
-!- MISCELLANEOUS: EU also differs in the amidation states of resi 155, 166, 177, 195, 198, 269, and 272 and in the order of resi
                                                                                                                                                                MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J. Edelman G.M.;
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Biochemistry 9:3161-3170(1970).
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cyanogen bromide fragments H5-H7.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 136-329 (EU).
MEDLINE=71064025; PubMed=5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
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Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
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                                                                                                                             SEQUENCE OF 1-135 (MYELOMA PROTEIN EU)
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MEDLINE=81208100; PubMed=7236608;
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77070269; PubMed=826475;
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231 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 VYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLY
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Spleen;
MEDILNE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 50.9%; Score 1240.5; DB 1; Length 330; Best Local Similarity 86.4%; Pred. No. 4e-78; Matches 242; Conservative 7; Mismatches 12; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36106 MW; 3770EE106C2FA33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0RR-2004 (TrEMBLrel. 26, Last ann
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319
330 AA;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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K -> R (in GlM(3) marker).

FT devAR 003886.

D -> E (in GlM(non-1) marker).

FTIdevAR 003887.

L -> M (in GlM(non-1) marker).

/FTIdevAR_003888.
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Interchain (with heavy chain)
Interchain (with heavy chain)
                                                                                          EMBL, J00228, AAC85227.1; ALT_INIT.

PIR, A93433, GHHU.

PIR, A93433, GHHU.

PBB; 1AJ7; X-ray; H-1-101.

PDB; 1D51; X-ray; H-1-101.

PDB; 1D51; X-ray; H-1-101.

R PDB; 1D51; X-ray; H-1-101.

R PDB; 1D51; X-ray; H-1-101.

R PDB; 1D51; X-ray; A/B=106-329.

R PDB; 1FCC; X-ray; A/B=106-329.

R PDB; 1FCC; X-ray; A/B=106-329.

R PDB; 1FCC; X-ray; A/B=106-329.

R PDB; 1ICX; X-ray; A/B=10-320.

R PDB; 1IX; X-ray; A/B=107-330.

R PROSTIE; PSO0290; 1G_MHC; 2.

M AD-SETUCEURE; Direct procein sequencing; Glycoprotein; NON TER 1 Memonglobulin domain.

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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_KHC.
InterPro; IPR003565; Ig_V.
Pfant, PP07654; C1-eet; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequences.";
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M. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Dubkins R.F., Jordan H., Moore T., Max S.I., Wang J., Histeh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Staplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Antilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Antilalon D.K., Muzny D.W., Garcia A.M., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Samilus D.E., Schnerch A., Schein J.E., Scherction and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCPAPELLGGPSVFLFPPKRKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 469;
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86.4%; Pred. No. 6.3e-78;
iive 7; Mismatches 12; Indels
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051328; AAH51328.1; -.
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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InterPro; IRR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-eet; 3.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
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les 242; Conservative
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcarane P.H.,
Richards S., Worley K.C., Hale S., Garcarane P.H.,
Whiting M., Madan P.J., Madan A., Young A.C., Bevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Spleen;
Strauberg R.;
Submitted (MU-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053984; AAH53984.1; --
HSSP; P01857; IHZH.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VVLSPSHGIELSVGEKLVLNCTARTELNV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 GLMTKKNSTFV--RVHEK--DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 ----KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 CVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 CKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 GIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                          Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (ANG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BX640853; CAE45920.1; -- HSSP; P01861; 1ADQ.
                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                               78; Indels
                                                                                                                                                                                                                                                                                                                                                                            52121 MW; 9476EAE4COBFC447 CRC64;
    annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.9%; Score 1239.5; DB Best Local Similarity 61.6%; Pred. No. 7.5e-78; Matches 263; Conservative 25; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 AA
                                                                                                                                                                                                          INCEPPO, IPRO03599; IG.
INCEPPO; IPRO03599; IG.
INCEPPO; IPRO03597; IG. II.
INCEPPO; IPRO03006; IG_MHC.
INCEPPO; IPRO03596; IG_MHC.
INCEPPO; IPRO03596; IG_W.
Pfam; PF07654; Cl-set; 3.
SWART; SM00409; IG; 2.
SWART; SM00406; IG; 3.
SWART; SM00406; IG; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS0835; IG_LIKE; 4.
05-JUL-2004 (TrEMBLrel. 27, Last and
Hypothetical protein DKFZp686C11235
Name=DKFZp686C11235;
                                                                                                      SEQUENCE FROM N.A.
TISSUE-Human small intestine;
The German Human cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q6PYX1;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 LTHROTNTIID----
                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein SEQUENCE 473 AA;
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                                                                             NCBI_TaxID=9606;
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AC Q6PYX:
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Created) Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 PCPAPELLGGBSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 IIDGVTRSDQGLYTCAA----SSGLMT-----KKNSTFV--RVHEK--DKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 VYTLPPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPVLDSDGSFFLY
                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 348;
                                                                                                                                                                                                                         Zhu N.S., Chen Y.Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; ARS70731; AAS88328.1; -.
HSSP; P01887; LAA7.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR00710; Ig-like.
InterPro; IPR0031006; Ig-MC.
InterPro; IPR003597; Ig-C1.
InterPro; IPR003597; Ig-C1.
SMART; SMART; SMO0407; IGL1; 3.
PROSITE; PS50835; IG-LIKE; 3.
PROSITE; PS508395; IG-LIKE; 3.
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hepatitis B virus receptor binding protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 AA; 38162 MW; DD96C3D7E0BE5845 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.8%; Score 1237.5; DB 2;
86.1%; Pred. No. 7e-78;
ive 8; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: September 23, 2005, 17:17:04 Job time : 124 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 86.1
Matches 241; Conservative
                                                               Homo sapiens (Human)
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=9606;
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                Copyright
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September 23, 2005, 14:00:46; Search time 120 Seconds (without alignments) 1476.135 Million cell updates/sec Run on:

US-10-811-170-2

score: Title: Perfect (

1 MVSYWDTGVLLCALLSCLLL.......MHEALHNHYTQKSLSLSPGK 458 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003as:* A Geneseq 16Dec04:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Description	9	6	4	Abp52447 Modified	Abp52450 Flt1D2.Fl	ß	æ	Aay97592 Flt1 rece		Aay97591 Flt1 rece		Aay97593 Flt1 rece	Abp52446 Mutation	7	a	Aay97590 Flt1 rece	Abp52443 Mutation	Abp70840 MVP-B.pro	_	3 MVP-A	9 MVP-A	7 ticam(Abu07273 Human exp	Abw02188 Human IL-	Adp76035 AMIGO pol
ID	AAY97596	ABP52449	AAY97594	ABP52447	ABP52450	AAY97595	ABP52448	AAY97592	ABP52445	AAY97591	ABP52444	AAY97593	ABP52446	AAY97597	ABP52442	AAY97590	ABP52443	ABP70840	ABP70841	ABP70853	ABP70839	AAR48037	ABU07273	ABW02188	ADP76035
DB	4	Ŋ	4	S	S	4	Ŋ	4	ß	4	Ŋ	4	Ŋ	4	ស	4	S	9	9	9	9	N	9	7	80
Length	458	458	458	458	432	455	455	462	462	452	452	567	567	567	567	557	557	934	949	816	810	680	8	915	4
% Query Match	100.0	100.0	98.4	98.4	93.4	84.9	84.9	84.1		83.6	83.6	82.7	82.7	82.7	82.7	82.2	82.2	ö	ö	9	9	53.5	ë.	53.1	53.0
Score	2437	2437	2399	2399	2275.5	2069.5	2069.5	2049	2049	2038	2038	2015.5	2015.5	2014.5	2014.5	2003.5	2003.5	1726.5	1716	1627.5	1619.5	1304	1304	1293.5	9
Result No.	-	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Ada14289 Mutated M	Abw02191 Human IL-	Abb07681 MOG-Fc fu	Adal4265 Human imm	Adi03928 B7-L1-Ig	Abw02182 Human IL-		Adq07407 hCBE11/hB			Adq12188 huCBE11 m	Aau09817 Murine FG	•	Aay97172 Human FGF	Aay97170 Human FGF		_	_	Aay92206 Fusion po	Abw02179 Human cyt
ADA14289	ABW02191	ABB07681	ADA14265	ADI03928	ABW02182	ADP76033	ADQ07407	ADQ12184	ADQ07411	ADQ12188	AAU09817	ABW02185	AAY97172	AAY97170	ADP03590	ADH34696	AA019052	AAY92206	ABW02179
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388	915	388	388	555	900	609	731	731	735	735	594	900	497	622	581	631	489	910	910
53.0	53.0	52.9	52.9	52.9	52.9	52.7	52.7	52.7	52.7	52.7	52.6	52.6	52.5	52.5	52.5	52.5	52.4	52.3	52.3
1290.5	1290.5	1289.5	1289.5	1289.5	1288	1285.5	1284.5	1284.5	1284.5	1284.5	1281.5	1281.5	1280	1279.5	1279	1279	1277.5	1275.5	1275.5
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region.
                                    Flt1 receptor fusion protein VEGFR1R2-FcDeltaC1(a).
         AAY97596 standard; protein; 458 AA.
                           entry)
                          (first
                           05-APR-2001
                  AAY97596;
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WO200075319-A1. Unidentified.

14-DEC-2000.

23-MAY-2000; 2000WO-US014142. 99US-0138133P. (REGE-) REGENERON PHARM INC. 08-JUN-1999;

Yancopoulos GD; Davis S, WPI; 2001-071076/08. N-PSDB; AAA91076. Papadopoulos NJ,

Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model systems.

Claim 49; Fig 24; 159pp; English.

This sequence represents a fusion protein of the invention between the Plt1 receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal

Sequence 458 AA;

Query Match

100.0%; Score 2437; DB 4; Length 458;

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administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region.
                                       Example 20; Fig 24A-C; 179pp; English
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nes 458; Conservative
                                                                                                                                                                                                                                   Sequence 458 AA;
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                     antagonist
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                                                                               120
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                                                                                                                                                                                                                                                                                                TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
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                                                 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT
                                                                                                                     HRQTNTII DVVLSPSHGI ELSVGEKLVLNCTARTELNVGI DFNWEYPSSKHQHKKLVNRD
                                                                                                                                HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD
                                                                                                                                                                                                                                                              KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
                                                                                                                                                                                                                                                                                    TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
                                                                                          LKTOSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC
                                                                                                                                                                               LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC
                                                                                                                                                                                                     PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                                                                                                                                                                                       PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                                                                                                                                                                                                           KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
                                      MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEI I HMTEGRELVI PCRVTS
                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified Flt1 receptor VEGFR1R2-FcDELTAC1(a) protein sequence.
                  Indels
                                                                                                                                                                                                                                                                                                                                        LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
        No. 1.1e-153;
                   Mismatches
        Pred.
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100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-2002; 2002WO-US002466
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                   458; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetic retinopathy
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       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABQ74610
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antianthamatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, rephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering CVEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with injury, oedema casociated with inflammatory disorders (e.g. rheumator) as age-related casthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2437; DB 5;
100.0%; Pred. No. 1.1e-153;
ive 0; Mismatches 0;
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240 300 300

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(first entry)

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ABP52447 standard; protein; 458 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKBIGLLTCEATVNGHLYKTNYLT 117
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                                                                                                                                                                                                                                                                                                               This sequence represents a fusion protein of the invention between the Fl1 receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Fl11 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                     Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.4%; Score 2399; DB 4; Length 458; 98.7%; Pred. No. 3.9e-151; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                         Yancopoulos GD;
                                                                                                                                                                                                                                                                                        Claim 49; Fig 21; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 vascular permeability in a mammal
                                                                           23-MAY-2000; 2000WO-US014142.
                                                                                                                               (REGE-) REGENERON PHARM INC
                                                                                                                                                         Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455; Conservative
                                                                                                                                                                                2001-071076/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                         Papadopoulos NJ,
                                                                                                                                                                                            N-PSDB; AAA91074
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 458 AA;
                       WO200075319-A1
Unidentified.
                                                                                                     08-JUN-1999;
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, espirotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents
                                                                                   psoriasis; wound healing; Flit receptor; antipsoriatis; antiinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory; ophthalmological; vascular permeability; oedema; inflammation; asthma; barin oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
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                                                              Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF)
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Modified Flt1 receptor Flt1D2.Flk1D3.FcDELTAC1(a) protein sequence.
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Pred. No. 3.9e-151;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 17; Fig 21A-C; 179pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yancopoulos GD;
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98.7%;
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                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antagonist.
                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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administrating a vacular endochelial cell growth factor (VEGF) antegonist to the mammal or human. A VEGF antagonist has antipsoriatic, antiarthatic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory discases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents
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 comprises
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                                                                                                                                                                                                                                                                                                                              Length 432;
wound healing in a mammal or a human. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flt1 receptor fusion protein Flt1D2.VEGFR3D3.FcDeltaC1(a)
                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                            Score 2275.5; DB 5;
Pred. No. 5.8e-143;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                            93.4%;
ilarity 99.3%;
Conservative
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Best Local Similarity
Matches 429; Conserv
                                                                                                                                                                                                                                                                                              Sequence 432 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, Flt1, vascular endothelial growth factor; VEGF; VEGF antagonist, psoriasis; wound healing; Flt1 receptor; antipsoriatic; antinflammatory; vulnerary; antiasthmatic; antinheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
HRQINTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
                 HRQINTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 177
                                                                LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
                                                                                    LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC 237
                                                                                                                                     297
                                                                                                                                                        PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
                                                                                                                                                                                                                           QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                                                                                                                                                         AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                     PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for treating psoriasis
                                                                                                                                                                                                                                                                                                                                                                YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flt1D2.Flk1D3.FcDELTAC1(a) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 28; Fig 36; 179pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2001; 2001US-00773877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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diabetic retinopathy.
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Disulfide-bond
Disulfide-bond
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Synthetic.
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23-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVYTLPPSRDELTKNQVSLTCLVXGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354
                                                                                                                                                                                                            This sequence represents a fusion protein of the invention between the Flt1 receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides were preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or
                                                                                                                                                                                                                                                                                                                                                                              1 MVSYWDIGVILCALISCLILIGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVIS 57
                                                                                                                                     Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                                                                                                                                                                                                                                  MVSYMDTGVLLCALLSCLLLTGSSSGSDTGRPFVBMYSEIPEIIHMTEGRELVIPCRVTS
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                                                                                                                                                                                                                                                                                                                          DB 4; Length 455;
                                                                                                                                                                                                                                                                                                                                              41; Indels
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                                                                                                                                                                                                                                                                                                                        84.9%; Score 2069.5; DB
85.7%; Pred. No. 3e-129;
ive 16; Mismatches 4:
                                                                                    9
                                                                                     Yancopoulos
                                                                                                                                                                                                                                                                                vascular permeability in a mammal
                                                                                                                                                                                          Claim 49; Fig 22; 159pp; English.
                      2000WO-US014142,
                                          99US-0138133P
                                                              (REGE-) REGENERON PHARM INC
                                                                                   Davis S,
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                        WPI: 2001-071076/08
                                                                                                                                                                                                                                                                                                                                   al Similarity
395, Conserv
                                                                                   Papadopoulos NJ,
                                                                                                                     N-PSDB; AAA91075
                                                                                                                                                                                                                                                                                                     Sequence 455 AA;
                     23-MAY-2000;
                                          08-JUN-1999;
 14-DEC-2000
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ABP52448 standard; protein; 455

ABP52448

RESULT 7
ABP52448
ID ABP5
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AC ABP5
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chancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipocriatic, antiantlammatory, vulnerary, antiathmatic, antiarheumatic, antianthratic, antiantlammatory, vulnerary, antiathmatic, antiarheumatic, antianthratic, comprises and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents
                                                           psoriasis, vuccusus enuounessas growth factor; VEGF; VEGF antagonist; psoriasis; antinifalammatory; vulnerary; antiasthmatic; antinifalammatory; ophthalmological; vascular permeability; oedema; inflammation; asthma; brain oedema; inflammation; asthma; kidney disease; eye disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration; diabetic retinopathv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRQINTIIDIQLLPRKSLELLVGEKLVINCTVWAEFNSGVTFDWDYPGKQAERGKWVPER 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF)
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Modified Flt1 receptor Flt1D2.VEGFR3D3.FcDELTAC1(a) protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes a method for treating psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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Best Local Similarity 85.7%
Matches 395; Conservative
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                                                                                  297
                                                                                                                                                                                   357
                                                                                                                                                                                                                AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 354
                                                                                                                                                                                                                                                                                                               This sequence represents a fusion protein of the invention between the Fli receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably FliI receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
     PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                   AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                  PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region.
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84.2%; Pred. No. 7.1e-128;
ive 13; Mismatches 47; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                           YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 455
                                                                                                                                                                                                                                                                                                                                                                                    YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flt1 receptor fusion protein Mut3:Flt1(2-3)-Fc.
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Matches 393; Conservative
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N-PSDB; AAA91072.
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1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS

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Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist; psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; opthialmological; vascular permeabliity; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration; diabetic retinopathy.
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                                               PNITVILKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT
                                                                                                                                                                                                                                                                                                                                                        PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT
                                                                                                                                                      121 HRQINTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                 181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutation 3 Flt1(2-3)-Fc protein sequence.
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipacriatic, antiarthritic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering vEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related maching the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present invention
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                                                                                                                                                                                                                                                                                                                                           $; Score 2049; DB 5;
8; Pred. No. 7.1e-128;
13; Mismatches 47;
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Best Local Similarity 84.2
Matches 393; Conservative
                                                                                                                                                                                                                                                                                                            Sequence 462 AA;
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                                                                                                                                                                                                                                                                                                     This sequence represents a fusion protein of the invention between the Fl1 receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides re preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.6%; Score 2038; DB 4;
83.9%; Pred. No. 3.7e-127;
iive 10; Mismatches 41;
                                                                                                                      Papadopoulos NJ, Davis S, Yancopoulos GD;
                                                                                                                                                                                                                                                                           Claim 49; Fig 14; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     vascular permeability in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP52444 standard; protein; 452
                            23-MAY-2000; 2000WO-US014142.
                                                           99US-0138133P
                                                                                        (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                   WPI; 2001-071076/08.
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Matches 392; Conserv
                                                                                                                                                                     N-PSDB; AAA91071
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 452 AA,
                                                           08-JUN-1999;
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346 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 405
166 EIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSC 225
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                                                                                                                                                                  286 GVEVHNAKTKPREEQYNSTYRVVSVLTVIHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                          226 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                               DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                          292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKÇKVSNKALPAPIEKTISKAK
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plasma leakage; vascular permeability; IgG Fc region.
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14; Mismatches 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY97593 standard; protein; 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-071076/08.
N-PSDB; AAA91073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 567 AA;
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Matches 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present line interests and an annual or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the manmal or human. A VEGF antagonist has antipsoriatic, antiarthritic, antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents Mutz.Fit(2-3 delta B)-Fc which is used in an example from the present invention
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                                                                                        Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist; psoriasis; wound healing; Flt1 receptor; antipsoriatic; antinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK------ 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes a method for treating psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutation 2 Flt1(2-3 delta B)-Fc protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2038; DB 5;
Pred. No. 3.7e-127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sxample 12; Fig 14A-C; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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  (first entry)
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                                                                                                                                                                                                             kidney disease; eye
diabetic retinopathy
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Best Local Similarity
Matches 392; Conserv
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DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 358
                                                                                                                                                                                                                                                   SVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNS 418
                                                                                                                                                                                                                                                                                                psoriasis; wound healing; Plt1 receptor; antipsoriatic, antinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeablity; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
                                                                                                                                                                                                                                    SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
                                                                                                                                                                                                                                                                                   TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
                                                                                                                                                                                                                                                                                                                                 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
                      61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
                                                                                           GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI
                                                                                                                                        ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI
                                                                                                                                                                                       DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK-----DKTHTCPPCPAPELLGGP
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N-PSDB; ABQ74607.
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Synthetic.
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antinflammatory, vulnerary, antiastehmatic, antiaheumatic, antianthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering veder antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injural society associated with injural, associated with injural, associated with injural associated with materials, asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents Mut4:Flt1(2-3 R
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                                                                                                                                          enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic,
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               Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SDTGRPFVEMYSEIPBIIHMTBGRELVIPCRVTSPNITVTLKKFPLDTLIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ESAIYIFISDTGRPFVEMYSEIPBIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                         present invention describes a method for treating psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.7%; Score 2015.5; DB 5; Length 567; 69.6%; Pred. No. 1.5e-125; ive 14; Mismatches 46; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                        ->N)-Fc which is used in an example from the present invention
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                                                                                      Example 14; Fig 16A-D; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 396; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 567 AA;
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RESULT 14 AAY97597

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enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antinflammatory, vulnerary, antiasthmatic, antiheumatic, antiarthritic, nephrocropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and
                                                                                                                                                                                                       479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeablity; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                               419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                            359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                        310 TYRVVSVLTVIHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                370 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes a method for treating psoriasis and
                                                                                                                                                                                                                                                                     430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                               539 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; Fig 10A-D; 179pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                            ABP52442 standard; protein; 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flt1(1-3)-Fc protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-2002; 2002WO-US002466.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGE-) REGENERON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetic retinopathy.
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ABP52442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a fusion protein of the invention between the Pt1 receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Fl11 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BSAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKPLDTLIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRR--IDQSNSHANIFYSVLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK-----DKTHTCPPCPAPELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SDIGRPFVEMYSEIPEIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                             Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
plasma leakage; vascular permeability; IgG Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.7%; Score 2014.5; DB 4. 69.6%; Pred. No. 1.8e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVSYWDTGVLLCALLSCLLLTGSSSG-----
                                                                                                                                    Flt1 receptor fusion protein Flt1(1-3)-Fc.
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AAY97597 standard; protein; 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Papadopoulos NJ, Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGE-) REGENERON PHARM INC
                                                                                        (first entry)
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Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-071076/08.
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                                                                                     05-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                       TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
                                                                                                                                         61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET 120
                                                                                                                                                                      BLSVGEKLVLNCTARTELAVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
                                                                                                                                                                                                                                                                                                                                                              -----SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKRPLDTLIPD 78
or vascular permeability. The present sequence represents Flt1(1-3)-Fc which is used in an example from the present invention
                                                                 Gaps
                                                                                   · 1 MVSYWDTGVLLCALLSCLLLTGSSSG--------
                                                                47; Indels 113;
                                              Length 567;
                                              DB 5;
                                             82.7%; Score 2014.5; DB 969.6%; Pred. No. 1.8e-125; tive 13; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                       QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567
                                                                                                                                                                                                                                                                                                                                                                                                                              OGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                            Query Match
Best Local Similarity 69.6*
Matches 396; Conservative
                           Sequence 567 AA;
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Search completed: September 23, 2005, 17:14:53 Job time : 125 secs

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OM protein - protein search, using sw model

September 23, 2005, 16:52:28; Search time 39 Seconds (without alignments) 1129.930 Million cell updates/sec Run on:

US-10-811-170-2 2437 Title: Perfect score:

1 MVSYWDTGVLLCALLSCLLL.......MHEALHNHYTQKSLSLSPGK 458 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		gamma-			ס	ש	g gamma-3	gamma-4	g gamma-3	מ	ь	Ig gamma 2a chain	מ	g gamma 4	g gamma 1	b	g gamma	ס	gamma-3 chai	g gamma-1		onoclona		b		b	ש	ס	וטו	
SUMMARIES		GHHU	869339	S31866	PT0207	G2HU	A23511	G4HU	A60764	G3HUWI	147160	147159	GHRB	147162	147158	G2GP	147161	S22080	G3MSC	S31459	G3MSM	PC4436	C30554	PS0018	S37483	G2MSA	G1MS	G2MSAM	S00847	PS0017
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Length		330	374	255	234	326	377	327	377	289	328	328	323	277	328	329	328	470	329	472	398	444	308	333	469	330	324	399	329	326
* Query Match		0	50.9	50.6	48.4	47.1	47.0	46.9	46.9	46.0	38.1	38.1	38.0	•	37.5	•	36.9	35	35.6	ო	٣	35.1	35.0	34.6	34.6	34.4	34.2	34.2	34.1	34.1
Score		1240.5	1240.5	1233	m	1148.5	1146	1144	1144	N	929.5	929.5	925.5	. 917.5	913.5	006	899.5	870	866.5	863.5	855.5	854.5	852	844	843.5	837.5	833.5	32.	832	831.5
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Ig gamma-1 chain C Ig gamma-2a chain Ig qamma-2a chain		soluble vascular e protein-tyrosine k Iq qamma-2b chain	Ig gamma-2 chain C protein-tyrosine k Ig gamma heavy cha	Fit-1 tyrosine kin receptor tyrosine	embryonic receptor Ig heavy chain V-I
G1MSM S40295 G2MSAB	G2MS11 PS0019 G2MSBM	A49636 S09982 S01321	S06611 JC1402 I46732	I60598 I78875	S49010 A36040
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39 446 335	474 322 405	687 1338 475	327 1356 180	1336	1330 218
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828.5 827 825	809 807.5 803.5	801.5 801.5 793	771.5	700.5	653.5 582.5
30 32	333 354 35	3.6 3.7 88	39 4 4 0 1	42	4 4 5

ALIGNMENTS

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RESULT 1
GHMU

GHMU

C; Species: Homo sapiens (man)
C; Species: J1-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
C; Date: J1-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
C; Date: J1-Jan-1981 #sequence of L.E.
R:Ellison, J.W.; Berson, BJJ; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
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A; Reference number: A93433; MUID:82274238; PMID:6287432

A, Molecule type: DNA

marker, 97-Lys, and the Glm(1) markers, A, Residues: 1-330 <-ELL>
A, Cross-references: UNIPROT: P01857; EMBL: Z17370
A, Note: Lhis sequence has the Gim(17) allotypic of A, Note: Lys-330 is removed after translation R, Harris, L.J.
submitted to the EMBL Data Library, October 1992
A, Reference number: S33904

A,Accession: \$36861 A,Molecule type: DNA A,Residues: 2-330 <HAR> A,Cross-references: EMBL:217370

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6211 29, 671-679, 1982
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A;Accession: S33887

A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:271370
B;Cross-references: EMBL:271370
B;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C.B.;Chemistry 9, 3161-3170, 1970
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A;Contents: myeloma protein Eu
A;Accession: B90563

A;Molecule type: protein
A;Mesidues: 1-56, R., 98-135 <CUN>
A;Residues: 1-56, R., 98-135 <CUN>
A;Note: this sequence has the Glm(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
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A,Molecule type: protein
A,Residues: 136-154, Q',156-165, Q',167-176, Q',178-194, N',196-197, D',199-238, E',240,
A,Residues: 136-154, Q',156-165, Q',167-176, Q',178-194, N',196-197, D',199-238, E',240,
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A;Accession: S69339  
A;Accession: S69339  
A;Cross-references: EMBL:X81695  
A;Cross-references: EMBL:X81695  
A;Cross-reference number: $72664  
A;Reference number: $72664  
A;Accession: $726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 274
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-140, (C', 142-374 <KH2>
A;Coss-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Best Local Similarity 72.9%; Pred. No. 1.5e-71;
Matches 248; Conservative 17; Mismatches 50.
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A,Molecule type: mRNA
A,Residues: 1-255 <FIL>
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A/Molecule type: protein
A/Accession: B91668
A/Molecule type: protein
B/Schmidt, W.E.; Jurg, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A/Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A/Accession: A/A1723
A/Molecule type: protein
A/Accession: A/A1723
A/Molecule type: protein
A/Accession: A/A1723
A/Molecule type: protein
A/Residues: 1-96, 'R', 98-197, 'D', 199-238,'E', 240, 'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Molecule type: protein
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Molecule type: protein
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Molecule type: protein
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Molecule type: protein
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Molecule type: protein
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Molecule type: protein
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Molecule type: protein
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 cSCE
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 199-286,'D', 199-286,'B', 1970
A/Residues: 1-96,'R', 98-197,'D', 199-238,'E', 1970
A/Residues: 1-96,'R', 1910-1910,'D', 190-1910,'D', 190-1910,'D', 190-1910,'D', 190-1910,'D', 190-1910,'D', 190-19
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Access references: GDB:120085; OMIM:147100
Access references: GDB:120085; OMIM:147100
Access references: GDB:120085; OMIM:147100
Access references: 940; 11441; 22471
Access references: 940; 11441; 22471
Access references: 940; 11441; 22471
Access references: 940; 11441; 12441
Access references: 940; 11441; 12441
Access references: 940; 11441; 12441
Access references: 940; 11441; 14451
Access references: 940; 1
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                                                                                                                                         A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
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C; Genetics:
A; Gene: GDB:IGHG1
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Gaps

25;

Indels

Length 374;

DB 2; 20; 238

94

154

298

214

358

418

334

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Ig gamma-1 chain C region - synthetic C;Species: synthetic C;Species: synthetic how sapiens (man) gene engineered and expressed in Escherichia coli A;Note: Howo sapiens (man) gene engineered and expressed in Escherichia coli C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000 C;Accession: S31866 Fishipula, D. Submitted to the EMBL Data Library, February 1993 A;Description: Screeing method for protein-protein interactions of cloned gene products. A;Reference number: S31866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069 C;Keywords: immunoglobulin F;1-22/Region: Escherichia coli outer membrane protein A precursor F;23-255/Region: human Ig gamma-1 chain C region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.6%; Score 1233; DB 4; Best Local Similarity 100.0%; Pred. No. 2.9e-71; Matches 227; Conservative 0; Mismatches 0;
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Ig heavy chain V region precursor - human C;Species: Homo sapiens (man)

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A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19, Q',21-57,2'.59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
A;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem: 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a A;Contents: myeloma protein Zie
A;Contents: myeloma protein Zie
A;Contents: myeloma protein Zie
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-7,A;Note: this sequence has since been revised
A;Note: this sequence has since been revised
A;Note: this sequence has since been revised
A;Note: this munol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin gs
A;Contents: Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
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A;Cross-references: GDB:119338; OMIM:147110
A;Cross-references: GDB:119338; OMIM:147110
A;Cross-references: GDB:119338; OMIM:147110
A;Cross-references: GDB:119338; OMIM:147110
A;Cross-references: GDB:133-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.32-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.34-14q32.33-14q32.34-14q32.33-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.34-14q32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 TPPAVLQS-SGLYSL---SSVVTVPSSNPGTQTYTCNVDHKPSNTKVDKTVERKCCVECP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A; Tile: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A; Reference number: A90253; WIDD:72033500; PMID:4940472
A; Contents: annotation; myeloma protein Sa, disulfide bonds
B; Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1569
A; Title: Structural studies of immunoglobulin G.
A; Reference number: A93157; MID:69064124; PMID:5782707
C; Genetics: annotation; Sa, disulfide bonds
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80.0%; Pred. No. 9e-66;
tive 13; Mismatches 20; Indels 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Accession: A93132
A/Accession: A93132
A/Molecule type: protein
A/Residues: 238-275 <HOF>
S.Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
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Best Local Similarity 80.03
Matches 224; Conservative
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C;Species: Homo sapiens (man)
C;Accession: A93966; A92809; A90752; A93132; A02148
R;Ellison, J; Hood, L.
A;Filison, J;Filison, L.
A;Filison, J;Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Immunol. 125, 1048-1054, 1980
A, Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
                                                                                                                                                                                                                                                                                89 GVEVHNAKTKPREEQYNSTYRVVSVLTVLAQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148
                                                                                                                                                                                                                                                                                                                                                                                                            DKTHTCPPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTPPVLDS 194
                                  DKTHICPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
                                                                                                                                                                                                                         GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graces: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207
A;Reference number: PT0207
A;Reference number: PT0207
A;Residues: 1-234 <=HRNA
A;Residues: 1-234 <=HRNA
A;Residues: 1-234 <=HRNA
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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                                                                                         DKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVUDVSHEDPEVKFNMYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 234;
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48.4%; Score 1180; DB 2; Length 2
Best Local Similarity 98.6%; Pred. No. 6e-68;
Matches 217; Conservative 1; Mismatches 2; Indels
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A; introns: 99/1; 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulface bonds. In some cases, such as IgA and IgM, the subunits associate into land disulface bonds. In some cases, such as IgA and IgM, the subunits associate into land; superfamily: immunoglobulin cargion; immunoglobulin homology c; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology <IM1>
F;90-110/Region: hinge F;340-203/Domain: immunoglobulin homology <IM2>
F;144-203/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;140-1301/147-305/Disulfide bonds: interchain (to heavy chain) #status experimental
F;27-83, 141-201, 247-305/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 TFPAVLQS-SGLYSLSSVVTVPSSSLGTKTYTCNVD-HKPSNTKVDKRVESKYGPPCPSC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 TLPPSOGEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSR 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 DIPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
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Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl,
A;Reference number: A60764; MUID:90007613; PMID:2571587
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                                                                      OMIM: 147130
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:08N4Y9
                                                                  A,Cross-references: GDB:119340; ON
A;Map position: 14q32.33-14q32.33
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nes 222; Conservative
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Best Local Similarity
Matches 210; Conserv
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                                    Gene: GDB:IGHG4
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                                                                                                                                                                                                           RESULT 6
A2351
Iggard 3
A2351
Iggard 3
A2351
Iggard 3
A2351
Iggard 4
A2351
Iggard 5
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C; Accession: A2351
R; Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A; Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A; Reference number: A23511; MUD:86148507; PMID:3081877
A; Reference number: A23511; MUD:86148507; PMID:3081877
A; Residues: 1-377 - cHUC>
A; Residues: 1-377 - cHUC>
A; Residues: 1-377 - cHUC>
A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics:
A; Gene: GBB:IGHG3
A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics:
A; GB:IGHG3
A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 20-65/Domain: immunoglobulin homology < IMM>
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A. Molecule type: DNA

A. Fesidues: 1-37 & ELL.

A. Fresidues: 1-30 & ELL.

A. Fresidues: 1-30 & ELL.

A. Fresidues: 1-30;81-35 & ELL.

A. Fresidues: 1-30;81-326 & Fernial amino acid sequence of the constant A. Reference number: A90249; MVID:70207560; PMID:4192699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 GVEVHNAKTKPREEGYNSTFRVVSVLTVLAQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
227 VYTLPPSREEMTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLY 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 GQPREPQVYTLPPSREEMTXNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 330
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G4HU

G9 gamma-4 chain C region - human

G species: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004

G sAccession: A90933; A90249; A02150

R FEllison, J ; Buxbaum, J ; Hood, L.

DNA 1, 11-18, 1981

A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGSPFLYSKITVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 47.0%; Score 1146; DB 2; Length 3 Best Local Similarity 92.5%; Pred. No. 1.5e-65; Matches 210; Conservative 8; Mismatches 9; Indels
                                                                                                    287 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
                                                               419
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380 VKGFYPSDIAVEWESNGO--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 437
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352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
Bixacskovics, I.; Sun, J.; Butler, J.B.
J. Immunol. 153, 3565-3573, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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R;Accession: 147160
R;Accession: 147160
R;Accession: 153, 3565-3573, 1994
J. Immunol. 153, 3565-3573, 1994
J. Immunol. 153, 3565-3573, 1994
J. Immunol. 163, 3655-3573, 1994
J. Reference number: 147158, MUID: 95015845; PMID: 7930579
J. Reference number: 147158, MUID: 95015845; PMID: 970579
J. Residues: 1928 kAC>
J. Cross-references: EMBL: U03780; NID: 9433125; PIDN: AAA52218.1; PID: 9433126
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                  184 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS
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                                                                                                                              GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;1133-202/Domain: immunoglobulin homology <IMM>
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56.1%; Pred. No. 7.2e
tive 41; Mismatches
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Best Local Similarity 56.1%;
Matches 180; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Igamma-3 heavy chain disease proteins - human C; Species: Homo sapiens (man) C; Species: 31-Dec-1979 # Sequence revision 23-Oct-1981 # text_change 16-Jul-1999 C; Accession: A90442; A02219; A90419; A90442; MID: 81021548; PMID: 6774747
A; Reference number: A90442; MID: 81021548; PMID: 6774747
A; Contents: heavy chain disease protein Wis A; Accession: A9042
A; Molecule type: protein A; A; Accession: A9042
A; Molecule type: protein A; A; Accession: A9042
A; Molecule type: protein A; A; Accession: A9042
A; Mote: the sequence of residues 42-76 was taken from the reference that follows R; Michaelsen, TE; Frandione, B; Franklin, B.C.
A; Mote: the sequence of residues 42-76 was taken from the reference that follows R; Michaelsen, TE; Frandione, B; Franklin, B.C.
A; Mote: the sequence of the 'hinge' region of human IgG3. Probable quadruplication A; Reference number: A92219; MUID: 77118561; PMID: 402363
A; Contents: normal gamma-3 chains; sequence corresponding to residues 12-97 of protein W A; Accession: A92219
A; Molecule type: protein A; A; Accession in gamma-3 chains is about four times as long as in other gamma in a comment (12-28)
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A,Nolecule type: protein lacks most of the V region, all of the CH1 region, and part of the A,Note: this protein lacks most of the V region, all of the CH1 region, and part of the R,Alexander, A.; Steinmetz, M. 79, 3260-3264, 1982
A,Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion A,Reference number: A93915; MUD:82247835; PMID:6808505
A,Contents: heavy chain disease protein Owm
A,Recession: A93915
A,Nolecule type: mRNA
A,Residues: 12-70,72-114;116-125, E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A,Note: a carboxyl-terminal Lys is removed posttranslationally
C,Comment: The heavy chain disease protein Wis is shown.
C,Genetics:
A,Gene: GBB:IGHG3
A,Gene: GBI-IGHG3
A,Gene: GBI-IGHG4
A,Gene: GBI-IGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form interpretentering at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form interpretented. To be a social sequence of Biochem. Biophys. Res. Commun. 71, 907-914, 1976

A.Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A.Reference number: A90199; MUID:77021516; PMID:823945

A.Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues A.Accession: A90198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                           271 GOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPVLDS 330
                                                    411
                                                    GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;103-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                46.0%; Score 1121; DB 1; Length 289; 90.3%; Pred. No. 4.3e-64;
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Sand Sounds

232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291

CDNA sequences of

us-10-811-170-2.rpr

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chain of rabbit immunoglobulin

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194 STLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPCP-APELLG-GPSV
                                   A;Title: Sequence studies of the Fd section of the heavy A;Reference number: A90245; MUID:70110015; PMID:5461106 A;Accession: A90245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig gamma chain C region - rabbit C; Species: Oryctolagus cuniculus (domestic rabbit)

C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 24-Apr. 1984 # Requence revision 15-Nov-1984 # text_change 09-Jul-2004
C; Accession: A91749; A90290; A93228; A94416; A02161
R; Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A; Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot
A; Reference number: A91749; MUID:84030930; PMID:6313520
A; Rolecule type: mRNA
A; Residues: 1.323 ABER>
A; Rolecule type: mRNA
A; Residues: 1.323 ABER>
A; Note: this sequence has the diz allotypic marker, 104-Thr, and the el4 marker, 185-Thr
R; Fratt, D.M.; Mole, L.E.
B; A; Title: Sequence studies on the constant region of the FG sections of rabbit immunoglob
A; Molecule type: protein
A; Reference number: A90290; MUID:76135469; PMID:1243651
A; Residues: 1-47, FE', 49-71, PV', 72-128 APR>
A; Molecule type: protein
A; Residues: 1-47, FE', 49-71, VPV', 79-6018-6022, 1982
A; Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A; Reference number: A93928; MUID:83299917; PMID:6193512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Cross-references: GB: MID: 18165111; PIDN: AAA31289.1; PID: 9155112
A; Note: this sequence has the dl1 allotypic marker, 104-Met, and the e15 allotypic marke
R; Fruchter, R.G.; Jackson, S.A.; Molle, L.E.; Porter, R.R.
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A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences A; Reference number: 147158; MUID:95015845; PMID:7930579
A; Accession: 147159
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-328 < KAC>
A; Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                    143 GEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTID 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 GVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DILMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSIYRVVSVLTV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 QHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEELSRSKVSITCL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 VIGEYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKASWQGGGIFQCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPNVALGCLASSYFPEPVTVTWNSGALSSGVHTFPSVL-----QPSGLYSLSSMVTVP
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                               Length 328;
                                                                                                                                                                                                                 A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                   83; Indels
                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                               Score 929.5; DB 2
Pred. No. 7.2e-52;
                                                                                                                                                                                                                                                                                                                            Query Match
38.1%; Score 929.5;
Best Local Similarity 56.1%; Pred. No. 7.2e
Matches 180; Conservative 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMHEALHNHYTQKSLSLSPGK 458
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Rosidues: 132-143, 'E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
A;Reference number: A94416
A;Reference number: A94416
A;Recession: A94416
A;Rosidues: 129-131;155-172, 'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'O','Z'
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapping infallide bonds. In some cases, such as 184 and 1894), the subunits associate into lang; Seywords duplication; alycoprotein; immunoglobulin homology
C;Keywords duplication; alycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology < IM2>
F;20-82/Domain: immunoglobulin homology < IM3>
F;20-82/Doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CjAccession: 14716;
RiKacskovics, I.; Sun, J.; Butler, J.E.
J. Immuol. 153, 3565-3573, 1994
A; Reference number: 147158; MUID: 95015845; PMID: 7930579
A; Reference number: 147158; MUID: 95015845; PMID: 7930579
A; Returns: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-277 < KAC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 TCPPPELLGGPSVFIFPPRFKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 TLTIDGV----TRSDQGLYICAA----SSGLMIKKNSTFVRVHEK-DKT---HTC--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 VYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.6%; Score 917.5; DB 2 nilarity 64.7%; Pred. No. 3.4e-51; Conservative 36; Mismatches 48
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Crossare references: UNIPROT: P01862
A; Crossare references: UNIPROT: P01862
B; Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
B; Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
A; File: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am)
A; Reference number: A90352; MUID: 71058471; PMID: 5538606
A; Molecule type: protein
A; Residues: 4-68 < BIR>
B; Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 197.
Biochemistry 10, 9-17, 197.
A; Fitle: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amir A; Fitle: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amir A; Fitle: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Accession: A90385
A Molecule type: protein
A Residues: 227-311 cTR2-
R Alesidues: 227-311 cTR2-
R A Residues: 227-311 cTR2-
R A Residues: 227-312 cTR2-
R A Residues: 227-312 cTR2-
R A Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A FReference number: A90354; MUID: 71058474; PMID: 4922544
A Contents: annotation; disulfide bonds
A Note: Cys-16 is involved in a heary-light chain bond
A Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
A Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp cycopreten); immunoglobulin crossists of two identical light (kapp hain disulfide bonds. In some cases, such as ISA and ISM, the subunits associate into la C; Superfamily: immunoglobulin homology
C; Keywords: duplication; glycoprofein; heterotetramer; immunoglobulin homology cIM1-
F; 21-91/Domain: immunoglobulin homology cIM2-
F; 21-310/Domain: immunoglobulin homology cIM2-
F; 21-310/Domain: immunoglobulin homology cIM3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: A90359
A,Molecule type: protein
A,Residues: 69-133/312-329 <TUR>
R,Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A,Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A,Reference number: A90384; MUID:75036072; PMID:4429665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from guinea pig IgG2 antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 SSQKA-----TCNVAHPASSTKVDKTVEPIRTPZPBPC-TCPKCPPPENLGGPSVFIFPP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GSMMTLGCLVKGYFPEPVTVKWNSGALTSGVHTFPAVL-----QSG--LYSLTSMVTVP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 GVTRSDQGLYTC-AASSGLMTKKNSTF--VRVHEKDKTHTCPPCPAPELLGGPSVFLFPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental
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C;Accession: A94553; A90352; A90359; A90384; A90385; A02151 R;Trischmann, T.M. submitted to the Atlas, April 1975 A;Reference number: A94553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Accession: A90384
A Modecule type: protein
A; Modecule type: protein
A; Residues: 134-226 < TRA>
B; Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A; Title: Primary structure of the C-H3 homology region f
A; Reference number: A90385; MUID:75036073; PMID:4609467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;28-79/Disulfide bonds: #status experimental
                                                                                                                                                                  A; Accession: A94553
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147158
167158
16 Jamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147158
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158; MUID:95015845; PMID:7930579
                                                                                                                                                                                                                                                                              SKYTLICLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKLAVDKASWQ 248
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                                                                                                                       143 GEKLVLNCTARTELNVGIDFNWE----YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTID 199
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                                                                                                                                                                                                                                    RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 371
                                                                                                                                                                                                                                                                                                                                                                                       NQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
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               16 SMVTVPASSLSSKS-YTCNVNHPATTTK-----VDKRVGTKTKPPCPICPACEGPGPSA 68
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C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 GPNVALGCLASSYFPEPVTVTWNSGALTSGVHTFPSVL-----OPSGLYSLSSMVTVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
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A,Gene: 1gdl
C,Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-128 <KAC>
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Matches 181; Conservative
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Search completed: September 23, 2005, 17:17:53 Job time : 41 secs

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                                                                                     2; Search time 45 Seconds (without alignments)
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2437
1 MVSYWDTGVLLCALLSCLLL......NHEALHNHYTQKSLSLSPGK
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/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-499-846-8
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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20, Appl
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NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: PAT ORGANISM: Artificial Sequence FEATURE:	; NUMBER OF SEQ ID NOS: 27 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 26 ; LENGTH: 458 ; TYPE: PRT ; ORGANISM: Artificial Sequence
CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: PRT CRGANISM: Artificial Sequence	CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SEQ ID NO 26 LENGTH: 458 TYPE: PRT ORGANISM: Artificial Sequence
CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: PRT CRGANISM: Artificial Sequence FEATURE:	CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: PatentIn version 3.0 ENGTH: 458 TYPE: PRT ORGANISM: Artificial Sequence
FILE REFERENCE: REG 710b CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: PatentIn version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: RT ORGANISM: Artificial Sequence FEATURE:	FILE REFERENCE: REG 710b CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SEQ ID NO 26 LENGTH: 458 TYPE: PRT ORGANISM: Artificial Sequence
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; FILE REFERENCE: REG 710b CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT PILLING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: PRT COGGANISM: Artificial Sequence FEATURE:	TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; FILE REFERENCE: REG 710b CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGHH: 458 TYPE: PRT ORGANISM: Artificial Sequence
APPLICANT: Xia, Yu-Ping et al. TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE. FILE REFERENCE: REG 710b CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: PRT CREANISM: Artificial Sequence FEATURE:	APPLICANT: Xia, Yu-Ping et al. TITLE OP INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE. TITLE OP INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE. CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: PATENTIN VERSION 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: PRT ORGANISM: Attificial Sequence
GENERAL INFORMATION: APPLICANT: Xia-Ping et al. TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE. TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE. CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: RT ORGANISM: Artificial Sequence FEATURE:	; GENERAL INFORMATION: ; APPLICANT: Xia, Yu-Ping et al. ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; ; TILE REFERENCE: REG 710b ; CURRENT APPLICATION NUMBER: US/09/773,877B ; CURRENT APPLICATION NUMBER: 2001-01-31 ; NUMBER OF SEO ID NOS: 27 ; SOFTWARE: Patentin version 3.0 ; SEO ID NO 26 ; LENGTH: 458 ; TYPE: PRT ; ORGANISM: Artificial Sequence
Patent No. 683349 GENERAL INFORMATION: APPLICANT: Xia, Yu-Ping et al. TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; FILE REFERENCE: REG 710b CURRENT APPLICATION NUMBE: US/09/773,8778 CURRENT PILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: PRT ORGANISM: Artificial Sequence FEATURE:	Fatent No. 6833349; GENERAL INFORMATION: APPLICANT: Xia, Yu-Ping et al. TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; FILE REFERENCE: REG 710b; CURRENT APPLICATION NUMBER: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGHH: 458 TYPE: PRT ORGANISM: Artificial Sequence
; Sequence 26, Application US/09773877B ; Patent No. 6833349 ; GENERAL INFORMATION: ; APPLICANT: Xia, Yu-Ping et al. ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; ; FILE REFERENCE: REG 710b ; CURRENT APPLICATION NUMBER: US/09/773,877B ; CURRENT FILING DATE: 2001-01-31 ; NUMBER OF SEQ ID NOS: 27 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 26 ; LENGTH: 458 ; TYPE: PRT ; ORGANISM: Artificial Sequence ; FEATURE:	; Sequence 26, Application US/09773877B ; Patent No. 6833349 ; GENERAL INFORMATION: ; APPLICANT: Xia, Yu-Ping et al. ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; ; CURRENT APPLICATION NUMBER: US/09/773,877B ; CURRENT FILING DATE: 2001-01-31 ; NUMBER OF SEQ ID NOS: 27 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 26 ; LENGTH: 458 ; TYPE: PRT ; ORGANISM: Artificial Sequence
US-09-773-877B-26 j. Sequence 26, Application US/09773877B j. Sequence 26, Application US/09773877B j. GENERAL INFORMATION: APPLICANT: Xia, Yu-Ping et al. TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; FILE REFERENCE: REG 710b CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: PRT FRATURE: PRATURE: FRATURE:	US-09-773-8778-26 j. Sequence 26, Application US/09773877B j. Patent No. 683349 j. GENERAL INFORMATION: APPLICANT: Xia, Yu-Ping et al. TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISE; TITLE OF INVENTION: WETHODS FOR TREATING INFLAMMATORY SKIN DISE; CURRENT APPLICATION NUMBER: US/09/773,877B CURRENT APPLICATION NUMBER: US/09/773,877B NUMBER OF SEQ ID NOS: 27 SOFTWARE: PatentIn version 3.0 SEQ ID NO 26 LENGTH: 458 TYPE: PRT ORGANISM: Attificial Sequence

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300 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT

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61 FIISNATYKEIGLLICEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLN 120
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Patent No. 6833349
GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 24
SEQ ID NO 24
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Pred. No. 7.5e-182;
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84.9%; Score 2069.5; DB

Best Local Similarity 85.7%; Pred. No. 1e-165;

Matches 395; Conservative 16; Mismatches 41
                                                                                                                                                                                                                                                                                    0; Mismatches
                    NUMBER OF SEQ ID NOS: 27
SOFWWARE: Patentin version 3.0
SEQ ID NO 27
EBNCTH: 431
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Local Similarity 99.1%;
les 428; Conservative C
                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                        OTHER INFORMATION: Peptide US-09-773-8778-27
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361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
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Patent No. 683349
GENERAL INFORMATION
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT APPLICATION NUMBER: US/09/773,877B
SOFTWARE: 201-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTING PATE: 201-01-31
SOFTWARE: PATENTING PATE: 201-01-31
SOFTWARE: PATENTING PATE: 201-01-31
SOFTWARE: ASS
LENGTH: 458
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APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 1707, 8778
CURRENT APPLICATION NUMBER: US/09/173, 8778
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Pred. No. 2e-193;
0; Mismatches 0; Indels
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                                                                     LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                          LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Best Local Similarity 98.7%;
Matches 455; Conservative
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-09-773-877B-22
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US-09-773-877B-27
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PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
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1 Sequence 16, Application US/09773877B

2 Sequence 17, Application US/09773877B

3 Fatent No. 683349

4 GENERAL INFORMATION:

APPLICANT: Xia, Yu-Ping et al.

7 TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

7 FILE REFERENCE: REG 710b

7 CURRENT APPLICATION NUMBER: US/09/773,877B

7 CURRENT FILING DATE: 2001-01-31

7 SOFTWARE: PATENTIN VOS: 27

7 SOFTWARE: PATENT VOS: 27

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US-09-773-877B-16
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                                                                                                              PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117
                                                                                                                                                                                  HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
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                                                                                 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
                                                                                                                                                                                                                                                                                                                                                                                         PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
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     1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS
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Sequence 18, Application US/09773877B

GENERAL INFORMATION:
APPLICANT: X1a, Yu-Ping et al.
TILLE OF INVENTION METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REF 710b

CURRENT FILING DATE: 2001-01-31

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.0

SEQ ID NO 18
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84.1%; Score 2049; DB 4;
Best Local Similarity 84.2%; Pred. No. 5.6e-164;
Matches 393; Conservative 13; Mismatches 47;
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ORGANISM: Artificial Sequence
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US-09-773-877B-18
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                                                                                                                                                                                                                                                                                                                   Gaps
                      Sequence 20, Application US/09773877B
Petent No. 6833349
GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILLE REPERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT APPLING DATE: 201-01-31
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 20
LENGTH: 567
                                                                                                                                                                                                                                                                                                                46; Indels 113;
                                                                                                                                                                                                                                                                                     Length 567;
                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                   82.7%; Score 2015.5; DB 4, 69.6%; Pred. No. 4.9e-161; Live 14; Mismatches 46;
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                                                                                                                                                                                                                                           OTHER INFORMATION: Flt1(1-3 R->N)-Fc (Mut4)
                                                                                                                                                                                                                                                                                                                                            1 MVSYWDTGVLLCALLSCLLLTGSSSG----
                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                              Best Local Similarity 69.6
Matches 396; Conservative
RESULT 7
US-09-773-877B-20
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US-09-773-877B-12
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Sequence 12, Application US/09773877B

Patent No. 6833349

GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
ATITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b

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121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 180
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Sequence 14, Application US/09773877B

Patent No. 6833349

GENERAL INFORMATION

TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

FILLE REFRENCE: REG 710b

CURRENT APPLICATION NUMBER: US/09/773,877B

CURRENT APPLICATION DATE: 2001-01-31

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 14

LENGTH: 557

LENGTH: 557
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CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVSYWDTGVLLCALLSCLLLTGSSSG
                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Flt(1-3)-Fc
US-09-773-877B-12
                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
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FEATURE
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                                                                                              Gaps
                                                                                            Indels 123;
                                                              DB 4; Length 557;
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Protein
                                                            Query Match
82.2%; Score 2003.5; DB 4
Best Local Similarity 69.4%; Pred. No. 4.9e-160;
Matches 395; Conservative 10; Mismatches 41;
             ; OTHER INFORMATION: Flt1(1-3 deltaB)-Fc (Mutl)
US-09-773-877B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Greve, Jeffrey M.
APPLICANT: Greve, Jeffrey M.
APPLICANT: McClelland, Alan
TITLE OF INVENTION: Multimeric Forms of Hun
TITLE OF INVENTION: Rhinovirus Receptor Pro
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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MEDIUM TYPE: diskette, 1.44 Mb storage COMPUTER: Dell Optiplex GX1
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 8.0 for Windows CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,496C
                                                                                                                              1 MVSYWDTGVLLCALLSCLLLTGSSSG-
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; Patent No. 6130202
; GENERAL INFORMATION:
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STATE: Connectic
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US-08-227-496C-15
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261 LTCAVILGNQSQETL--QTVTIXSPPAPNVILTKPEVSEGTEVTVKCE-AHPRAKVTLNG 317
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OTHER INFORMATION: amino acid residues 1-453 =
OTHER INFORMATION: tICAM(453); amino acid residues 454-680 = amino
OTHER INFORMATION: acid residues 216-442 of human IgG1 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 MKKFLSTLTIDG------VTRSDQGLYTCAASS--GLMTKKNSTFV-RVHEKDKT
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                                                                                                                                                                                                                                                                                                                                                                 214.2C
CLEASSIFICATION: 514

PRIOR SIPICATION DATA:
APPLICATION NUMBER: 07/903,069
FILING DATE: 06/22/92
APPLICATION NUMBER: 07/704,984
FILING DATE: 06/24/91
APPLICATION NUMBER: 07/556,238
FILING DATE: 07/20/90
ATTORNEY/AGENT INFORMATION:
NAME: Barbara A. Shimei
REGISTRATION NUMBER: 29,862
REFERENCE/DOCKET NUMBER: MTI 214
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2786
TELEPHONE: (203) 812-2786
TELEPHONE: (203) 812-5786
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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TYPE: amil
TOPOLOGY:
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US-09-499-846-6
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294 516 354 576 414 636

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53 ----
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US-09-313-942-28
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LENGTH: 910
US-09-499-846-2
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                                                                                                                                                                                                                                                                                                                                                                                                                             60 PSSGTPNPTLRWLK------NGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----EATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 IVENEYGSIN-HTYQ-----LDVVERSPHRPILQAG----LPANKTVALGSNV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 DFNWEYPSSKHQHKKLVN-------RDLKTQSGSEMKKFLSTLTIDGVTR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 EFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSF 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCPPCPAPELLGGPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 TCPPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 334
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                                                                                                                                                                                                                                                                                                                                                4 WKCLLFWAVLVTATLCTARPSPTLPEQP-VAPYWTSPE---KMEKKLHAVPAAKTVKFKC
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                           5 WDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVT-
                                                                                                                                                                                                                                                                                           98;
                                                                                                                                                                                                                                                         Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDQGLYTCAASSGLMTKKNSTFVRVHEK--------
                                                                                                                                                                                                                                                       Query Match 52.5%; Score 1280; DB 4; Length 4. Best Local Similarity 54.3%; Pred. No. 2.9e-99; Matches 284; Conservative 32; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 497
          APPLICANT: Kavanaugh et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASELSEQ for Windows Version 3.0
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Patent No. 6656728

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE: 035784/195012 (5784-
CURRENT APPLICATION WUMBER: US/09/499,846
CURRENT PILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 622
                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                   LENGTH: 497
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US-09-499-846-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 ERSPHRPILQAG----LPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 LPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 RPAVMISPLYLESRGGLVPRGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 KDTLMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLI 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 542
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                                                                                                                                                                                                                                                                                                                                                                                   87 R-KGFIISNATYKEI------GLLTC-----EATVNGHLYKTNYLTHRQTNTIIDVV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 LVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 438
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                                                                                                                                                                    95 DSGLYAC-----VTSSPSGSDTTYFSVNVSDALPSSEDDDDDDSSSEEKETDNTKPN
                                                                                                                                                                                                                                                                                                                                                                                                                             200 RIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSIN-HTYQ------LDVV
                                                                                                                                                                                                                                                         ----VIPCRVT-----SPNITVTLKKFPLDTLIPDGKRIIWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----RDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---
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                                                                                                                            6 DIGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIP-----EIIHMTEGREL----
                                                                 Gaps
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Patent No. 6472179
TITLE OF INVENTION: AND USING
TITLE OF INVENTION NUMBER: 08/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
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   Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 LSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVN----
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                                                                 Indels
   DB 4;
                                                              34; Mismatches 100;
Query Match 52.5%; Score 1279.5; DB Best Local Similarity 51.2%; Pred. No. 4.5e-99, Matches 287; Conservative 34; Mismatches 100
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHEALHNHYTQKSLSLSPGK 622
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Best Local Similarity 63.55
Matches 257; Conservative
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US-09-313-942-28
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OY 300 TKREEQTNSTRAVSULTUHODWINGGENERGAPERINESTS CARGOPERING D) 367 TKREEQTNSTRAVSULTUHODWINGGENERGAPERINE D) 427 TKLEEGTNSTRAVSULTUHOWINGGENERGAPERINE D) 427 TKLEEGTNSTRAVSULTUHOGENERGAPERINE D) 427 TKLEEGTNSTRAVSULTUKGFYEBDIAVEWESNGOPENNYKTTPPVLDSDGSFPLL D) 427 TKLEEGTNSTRAVSULTUKGFYEBDIAVEWESNGOPENNYKTTPPVLDSDGSFPLL D) 487 KLTVDKSRNQCANVESCSVMHEALHHYTOKSISLSPGK 525 RESULT 15 RESULT 15 RESULT 15 GENERAL INFORMATION: 1	161 DFNWEYPSSKHOHKKLVN 155 EFMCKVYSDPOPHIQWLKHIEVNGS 204 SDQGLYTCAASSGLMTKKUSTFVRV 215 EDAGEYTCLAGNSIGLSHHSAWLTV 245 LLGGPSVFLFPPKPKDTLMISRTPE 275 LEGGPSVFLFPPKPKDTLMISRTPE 305 EQYNSTYRVVSVLTVLHQDWLNGKE 315 EQYNSTYRVVSVLTVLHQDWLNGKE 316 SRDELTKNQVSLTCLVKGFYPSDIA 317 SRDELTKNQVSLTCLVKGFYPSDIA 318 SRDELTKNQVSLTCLVKGFYPSDIA 319 SRDELTKNQVSLTCLVKGFYPSDIA 310 SRDELTKNQVSLTCLVKGFYPSDIA 311
18 DGKRIIMDS	Ouery Match 52.3%; Score 1274.5; DB 4; Length 525; Best Local Similarity 59.0%; Pred. No. 9.2e-99; Matches 271; Conservative 25; Mismatches 78; Indels 85; Gaps 9; 60 SPNITVTLKKFPLDTLIPDGKRIHWDSR-KGFIISNATYKEIGLLTC 105

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EPQV 359 ||||| EPQV 426 FLYS 419 ||||| FLYS 486 ips 12; 11 105 | 105 | 111 | 111 | 111 XPRE 304 ||||| |XPRE 334 69 ----KFKC 59

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Sequence 26, App.
                                                                                                                                          September 23, 2005, 17:12:57; Search time 123 Seconds (without alignments) 1515.541 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                 1 MVSYWDTGVLLCALLSCLLL........MHEALHNHYTQKSLSLSPGK 458
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-609-775-10
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US-10-909-011-4
US-10-998-243-16
US-11-016-097-16
US-11-039-144-2
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                                                                                                                                                                                                                                                                                                                                                                                                                              1826521 seqs, 407012169 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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US-09-773-8774-26

Sequence 26, Application US/09773877A

Sequence 26, Application US/09773877A

Publication No. US20030017977A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

FILE REFERENCE: REG 710b

CURRENT APPLICATION NOSE: 2001-01-31

NUMBER OF SEQ ID NOS: 27
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Pred. No. 3.5e-152;
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100.0%; Score 2437;
Best Local Similarity 100.0%; Pred. No. 3.5
Matches 458; Conservative 0; Mismatches
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SEQ ID NO 26
LENGTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kandel, Jessica
APPLICANT: Holash, Jocelyn
APPLICANT: Yamashiro, Darrell
APPLICANT: Huang, Jianzhong
APPLICANT: Huang, Jianzhong
APPLICANT: Rudge, John
ITILE OF INVENTION: Method of Tumor Regression with VEGF
ITILE DE INVENTION: Inhibitors
FILE REFERENCE: REG 714A
CURRENT APPLICATION NUMBER: US/10/860,958
CURRENT APPLICATION NUMBER: 60/476,425
PRIOR PILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/476,425
PRIOR PILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO SEQ ID
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Matches 458; Conserv
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JAPPLICANT: Thomas J. Daly

APPLICANT: James P. Fandl

APPLICANT: James P. Fandl

APPLICANT: Nicholas J. Papadopoulos

TITLE OF INVENTION: UGEF TRAPS AND THERAPEUTIC USES THEREOF

FILE REFERENCE: REG 710D

CURRENT APPLICATION NUMBER: US/10/609,775

CURRENT APPLICATION NUMBER: US/10/009,852

PRIOR PILING DATE: 2001-12-06

PRIOR FILING DATE: 2001-12-06

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 1999-06-08

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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US-10-609-775-10
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; Publication No. US20050043236A1
; GENERAL INFORMATION:
    APPLICANT: Daly, thomas J.
; APPLICANT: Fandl, James P.
; APPLICANT: Fandl, James P.
; APPLICANT: Pandl, James P.
; APPLICANT: Pandl, James P.
; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof FILE REFERENCE: RGE 710D2
; CURRENT PAPLICATION NUMBER: US/10/880,021
; CURRENT FILING DATE: 2004-06-29
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS: 29
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100.0%; Score 2437; DB 17;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                        Query Match 100.0%; Score 2437; DB 17; Best Local Similarity 100.0%; Pred. No. 3.5e-152; Matches 458; Conservative 0; Mismatches 0;
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          PRIOR APPLICATION NUMBER: 60/493,971
PRIOR FILING DATE: 2003-08-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 458
  2004-07-23
                                                                                                                                                              TYPE: PRT
CRGANISM: homo sapiens
US-10-897-802-2
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-880-021-10
CURRENT FILING DATE:
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US-10~880-021-10
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Publication No. US20050032699A1
GENERAL INFORMATION:
APPLICANT: Jocelyn Holash
APPLICANT: Limin Hu
APPLICANT: Limin Hu
APPLICANT: Cacorge D. Yancopoulos
TITLE OF INVENTION: Composition of a VEGF Antagonist and an Anti-Proliferative Agent
FILE REFERENCE: REG 7158
CURRENT APPLICATION NUMBER: US/10/897,802
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                                                                                                                                                                                  APPLICANT: Stanley Wiegand
APPLICANT: Stanley Wiegand
APPLICANT: Jingtai Cao
APPLICANT: Jingtai Cao
APPLICANT: Jingtai Cao
TITLE OF INVENTION: Method of Treating Corneal Transplant
TITLE OF INVENTION: Method on
FILE REFERENCE: REG 713B
FULE APPLICATION NUMBER: US/10/830,902
CURRENT FILING DATE: 2004-04-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                Sequence 2, Application US/10830902; Publication No. US20050004027A1; GENERAL INFORMATION:
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LENGTH: 458
                                                                      RESULT 4
US-10-830-902-2
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US-10-897-802-2
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RESULT 8

US-10-988-243-16

US-10-988-243-16

Sequence 16, Application US/10988243

Publication No. US20050175610A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wiegand, Stanley

TILLE OF INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinectic Prop.

TILLE OF INVENTION: and Methods of Making and Using Thereof

TILLE OF INVENTION: MOMBER: 10/009,852

PRIOR APPLICATION NUMBER: 10/009,852

PRIOR APPLICATION NUMBER: PCT/US00/14142

PRIOR APPLICATION NUMBER: PCT/US00/14142

PRIOR APPLICATION NUMBER: 60/138,133

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/138,133

PRIOR FILING DATE: 1999-06-08

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 16

SEQ ID NO 16

INDERTH: 458
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    LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC
                          181 LKTQSGSBMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC
                                                                               PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
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ORGANISM: Homo sapiens
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Sequence 1.4 Application US/10909011

Publication No. US20050112061A1

Publication No. US20050112061A1

GENERAL INFORMATION:

APPLICANT: Jocelyn Holash

APPLICANT: Randy Burd

TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy

FILE REFERENCE: REG 716A

CURRENT PELING DATE: 2004-07-30

FRIOR PILING DATE: 2003-08-06

NUMBER OF SEQ ID NOS: 4

SOFTWARRE: FastSEQ for Windows Version 4.0

SEQ ID NO 4.0
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Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0; Indels 0;
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TITLE OF INVENTION: MODIFIED CHIMERIC POLYBETIDES WITH IMPROVED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REFERENCE: REG 710-A-US
CURRENT PEPLICATION NUMBER: US/11/016,097
CURRENT FILING DATE: 2004-12-17
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-33
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-33
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  421 LTVDKSRWQQGNVPSCSVMHEALHNHYTQKSLSLSPGK 458
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                                                                                                                             Sequence 16, Application US/11016097; Publication No. US20050163798A1; GENERAL INFORMATION:
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(WS-11-039-144-2)
Sequence 2, Application US/11039144
Publication No. US20050197291A1
GENERAL INPORMATION:
APPLICANT: Stanley Wiegand
APPLICANT: Jingtai Cao
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Matches 458; Conservative
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US-11-016-097-16
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APPLICANT: JOCCELYM Holash
APPLICANT: JOCCELYM Holash
APPLICANT: George Yancopoulos
APPLICANT: Adam P. Dicker
APPLICANT: Randy Burd
TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
FILE REFERENCE: 7168
CURRENT APPLICATION NUMBER: US/10/998,881
CURRENT APPLICATION NUMBER: 10/999,011
PRIOR APPLICATION NUMBER: 60/492,864
PRIOR APPLICATION NUMBER: 60/492,864
PRIOR PILING DATE: 2003-08-06
PRIOR FILING DATE: 2003-08-06
AUWHER OF SEQ ID NOS: 4
SOFTWARE: FRASESQ for Windows Version 4.0
                           TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
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100.0%; Score 2437; DB 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/10998881; Publication No. US20050196340A1; GENERAL INFORMATION:
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ORGANISM: homo sapiens
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LENGTH: 458
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Best Local Similaricy Matches 455; Conservative
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Best Local Similarity 98.7
Matches 455; Conservative
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CORGANISM: homo sapiens
US-10-609-775-8
                                         Query Match
Best Local Similarity
        US-09-773-877A-22
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US-10-609-775-8
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 458
APPLICANT: Claus Cursiefien
TITLE OF INVENTION: Method of Treating Corneal Transplant
TITLE OF INVENTION: Rejection In High Risk Keratoplasty Patients
FILE SEPERENCE: 713C
CURRENT PILING DATE: 2005-01-19
PRIOR APPLICATION NUMBER: 10/830, 902
PRIOR PILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2003-05-28
NUMBER OF SEQ ID NOS: 2
SOSTWARR: FREEEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Flt1D2.Flk1D3.FcdeltaC1(a) Receptor
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US-09-773-877A-22
Sequence 22, Application US/09773877A; Publication No. US20030017977A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 458; Conservative
                                                                                                                                                                                                                        LENGTH: 458
TYPE: PRT
ORGANISM: homo sapiens
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APPLICANT: Thomas J. Daly
APPLICANT: Jones P. Fandl
APPLICANT: Jones P. Fandl
FILE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
FILE REPRENCE: REG 7100
CURRENT FILING DATE: 2003-06-30
FRIOR APPLICATION NUMBER: 10/09,852
PRIOR PLING DATE: 2001-12-06
PRIOR PLING DATE: 2001-12-06
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/138,133
PRIOR PLING DATE: 1999-06-08
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 1995-06-08
SOFTWARE: FASTER OF NOS: 25
SOFTWARE: FASTER OF OF Windows Version 4.0
         Length 458;
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98.7%; Pred. No. 1.1e-149;
iive 0; Mismatches 0;
Score 2399; DB 10;
Pred. No. 1.1e-149;
                                                                  0; Mismatches
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         98.4%;
98.7%;
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Db 238 PPCPAPELLGGPSVFLFPPKPXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297 Qy 298 AKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357 L	RESULT 15 US-10-909-011-2 ; Sequence 2, Application US/10909011 ; Publication No. US20050112061A1 ; GENERAL INFORMATION: ; APPLICANT: Jocelyn Holash ; APPLICANT: George Yancopoulos ; APPLICANT: Adam P. Dicker ; APPLICANT: Randy Burd ; APPLICANT: Randy Burd ; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy ; FILE REFERENCE: REG 716A ; CURRENT APPLICATION NUMBER: US/10/909,011	CURRENT FILING DATE: 2004-07-30 PRIOR APPLICATION NUMBER: 60/492,864 PRIOR FILING DATE: 2003-08-06 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORCANISM: homo sapiens -10-909-011-2 Query Match Best Local Similarity 98.7%; Pred. No. 1.1e-149; Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps	1 1 61 58 121	HROTH'LIDVOLSPENGIELSUGEKUVLUCTARTELNGIEDENBEPESKHOHKKLUNKD HROTHTIDVOLSPENGIELSUGEKUVLUCTARTELNVGIEDENBEPESKHOHKKLUNKD HROTHTIIDVOLSPENGIELSUGEKUVLUCTARTELNVGIEDENBEPESKHOHKKLUNKE LKTOSGSEMKKFLSTLTIDGUTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTC	OY 238 PPCPAPELLCGPSVPL#PPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN 297	298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 358 QVYTLPPSRDELTKNQVSLTCLVKGFYFSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL	
61 PNITUTLKKEPLDTLIPDGKRIIMDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 1 58 PNITUTLKKEPLDTLIPDGKRIIMDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 1 121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELAVGIDFNWEYPSSKHQHKKLVNRD 1 118 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELAVGIDFNWEYPSSKHQHKKLVNRD 1 119 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELAVGIDFNWEYPSSKHQHKKLVNRD 1 181 LKTQSGSEMKKELSTLTIDGVTRSDQGLYTCAASSGLMTKKNSFFVRVHEKDKTHTC 2 111	Db 238 PPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297 Qy 298 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357	RESULT 14 US-10-880-021-8 Sequence 8, Application US/10880021 Sequence 8, Application US/10880021 GENERAL INFORMATION: APPLICANT: Daly, thomas J. APPLICANT: Fandl, James P. APPLICANT: Papadopoulos, Nicholas J. FILE REFERENCE: RGE 71002 CURRENT APPLICATION NUMBER: US/10/880,021 CURRENT APPLICATION NUMBER: 1004-06-29 PRIOR APPLICATION NUMBER: 10/609,775 PRIOR PILING DATE: 2003-06-30	NUMBER OF SEQ ID NOS: 29 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO8 LENGTH: 458 TYPE: PRT ORGANISM: homo sapiens S-10-880-021-8 Ouery Match 98.4%: Score 2399: DB 17:	Similarity 98.7%; Pred. No. 1.1e-149; 5; Conservative 0; Mismatches 0; Indels MVSYMDTGVLLGALLSCLLITGSSSGSDTGRPFVEMYSEIPEIIHWTE	CY 61 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120	118 HRQTNTIIDVVLSPSHGIBLSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 1 181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTC 2	N

418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458

Search completed: September 23, 2005, 17:21:05 Job time: 125 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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